

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:49:53 ; Search time 60 Seconds

(without alignments)
2316.890 Million cell updates/sec

Title: US-09-978-188a-7

Perfect score: 2527
Sequence: 1 MVKFFALTHWFLRLFLVLP.....TDMPTTEVTDIVEMREENE 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2527	100.0	492	2	AA41686 Human PRO
2	2527	100.0	492	3	AB44242 Human PRO
3	2527	100.0	492	5	AAU86135 Human PRO
4	2527	100.0	492	6	ABO25188 Novel hum
5	2527	100.0	492	6	ABU72194 Novel hum
6	2527	100.0	492	6	ABU84874 Human sec
7	2527	100.0	492	6	ABU61072 Human PRO
8	2527	100.0	492	6	ABU80341 Human sec
9	2527	100.0	492	6	ADA24546 Novel hum
10	2527	100.0	492	6	ABO19643 Novel hum
11	2527	100.0	492	6	ADA12207 Human sec
12	2527	100.0	492	6	ABO19534 Novel hum
13	2527	100.0	492	7	AD373513 Human PRO
14	2527	100.0	492	7	AD376229 Human PRO
15	2527	100.0	492	7	AD43655 Human sec
16	2527	100.0	492	7	AD361415 Human sec
17	2527	100.0	492	7	AD363379 Human sec
18	2527	100.0	492	7	AD366479 Human sec
19	2527	100.0	492	7	AD368603 Human sec
20	2527	100.0	492	7	AD362663 Human sec
21	2527	100.0	492	7	AD367728 Human sec
22	2527	100.0	492	7	AD441048 Human sec
23	2527	100.0	492	7	AD367103 Human sec
24	2527	100.0	492	7	AD362039 Human sec
25	2527	100.0	492	7	AD41672 Human sec

26	2527	100.0	492	7	AD49041 Human sec
27	2527	100.0	492	7	AD35095 Human sec
28	2527	100.0	492	7	AD36203 Human sec
29	2527	100.0	492	7	ADD72824 Human sec
30	2527	100.0	492	7	ADD72182 Human sec
31	2527	100.0	492	7	AD36833 Human sec
32	2527	100.0	492	8	AD48341 Human sec
33	2527	100.0	492	8	AD39442 Human sec
34	2527	99.8	492	4	AAU05581 Human pro
35	2522	99.8	492	5	ABB98306 Human ANK
36	2522	99.8	492	6	ABR57487 Human ANK
37	2514	99.5	492	5	ABB98316 Human ANK
38	2511.5	99.4	493	5	ABB98315 Human ANK
39	2510	99.3	492	5	ABB98312 Human ANK
40	2508	99.2	492	5	ABB98311 Human ANK
41	2507.5	99.2	491	5	ABB98313 Human ANK
42	2505.5	99.1	491	5	ABB98314 Human ANK
43	2502	99.0	492	4	AAU05582 Mouse pro
44	2502	99.0	492	5	ABB98307 Mouse ANK
45	2345	92.8	467	4	AA40539 Human pol

ALIGNMENTS

RESULT 1
AA41686
ID AA41686 standard; protein; 492 AA.

AC AA41686;
XX
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO274 protein sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
XX WO9946281-A2.
XX
PD 16-SEP-1999.
XX
XX 08-MAR-1999; 99WO-US005028.
XX
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-0004022O.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 27-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 31-MAR-1998; 98US-0080105P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080165P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 08-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 05-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085589P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR (GETH) GENENTECH INC.
XX PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX PI WPI; 1999-551358/46.
XX DR N-PSDB; RAZ33895.
XX DR
XX PT New secreted and transmembrane polypeptides and their polynucleotides,
XX PT useful for treating blood coagulation disorders, cancers and cellular
XX PT adhesion disorders.

XX Claim 12; Fig 4; 530pp; English.
PS The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to
CC AA41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX SQ Sequence 492 AA;
SQ Query Match 100.0%; Score 2527; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVRFPALTYWPLIRPLVPLGITNIALDFEQALNRGIAA VKEDAVEMLASVGLAYSLMK 60
Db 1 MVRFPALTYWPLIRPLVPLGITNIALDFEQALNRGIAA VKEDAVEMLASVGLAYSLMK 60
Qy 61 FFTGPMDSDFKNVGLVFNYSKRDRTKAVLCMVVAGAAIAA VFTHTLIAYSDLGYYIINKLHV 120
Db 61 FFTGPMDSDFKNVGLVFNYSKRDRTKAVLCMVVAGAAIAA VFTHTLIAYSDLGYYIINKLHV 120
Qy 121 DESVGSKTRAFILYLAAPFMDAMWATHAGILKHKYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVGSKTRAFILYLAAPFMDAMWATHAGILKHKYSFLVGCASISDVIAQVVFVAILL 180
Qy 181 HSHLECREPLLIPILSLYMGALVRCITTLCLGYGYNKIHDIIPDRSGPELGSDATIRKMLSF 240
Db 181 HSHLECREPLLIPILSLYMGALVRCITTLCLGYGYNKIHDIIPDRSGPELGSDATIRKMLSF 240
Qy 241 WWPLALILATQISRPITVNI FVSRDLGGSSAAEAVALITATYVGHMPYGMWTEIRAVY 300
Db 241 WWPLALILATQISRPITVNI FVSRDLGGSSAAEAVALITATYVGHMPYGMWTEIRAVY 300
Qy 301 PAFDKNPNKLVSTSNVTAAHIKFTFVCMALSLTLCFWMFTPNVSEKILIDIIGVD 360
Db 301 PAFDKNPNKLVSTSNVTAAHIKFTFVCMALSLTLCFWMFTPNVSEKILIDIIGVD 360
Qy 361 FAFALCVPLRIPSPFPVPTVRAHLTGWIMTKTFTVLAPSVLRILVLIASLVLPY 420
Db 361 FAFALCVPLRIPSPFPVPTVRAHLTGWIMTKTFTVLAPSVLRILVLIASLVLPY 420
Qy 421 LGVHGATLGVGSLLAGFVGSTWVAIAACVYRKQKKMENESATEGEDSAMTDMPTTE 480
Db 421 LGVHGATLGVGSLLAGFVGSTWVAIAACVYRKQKKMENESATEGEDSAMTDMPTTE 480
Qy 481 VTDIVEMRENE 492
Db 481 VTDIVEMRENE 492
RESULT 2
AAB44242
ID AAB44242 standard; protein; 492 AA.
XX AC AAB44242;
XX DT 08-FEB-2001 (first entry)
XX DE Human PRO274 (UNQ241) protein sequence SEQ ID NO:7.
XX KW Human; secreted protein; transmembrane protein; PRO; EST; cyrostatic;
XX KW expressed sequence tag; detection; cancer.
XX OS Homo sapiens.
XX XX WO200053756-A2.
XX PN

XX PD 14-SEP-2000.
XX PF 18-FEB-2000; 2000WO-US004341.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 12-MAR-1999; 99US-0123957P.
XX PR 29-MAR-1999; 99US-0126773P.
XX PR 21-APR-1999; 99US-0130232P.
XX PR 28-APR-1999; 99US-0131445P.
XX PR 14-MAY-1999; 99US-0134287P.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 16-DEC-1999; 99WO-US028565.
XX PR 30-DEC-1999; 99WO-US030095.
XX PR 30-DEC-1999; 99WO-US031243.
XX PR 05-JAN-2000; 99WO-US031274.
XX PR 06-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX DR WPI; 2000-611443/58.
XX DR N-PSDB; AAC78459.
XX PT Novel PRO polypeptides and polynucleotides used in detection methods, to
XX PT target bioactive molecules to specific cells, and to modulate cellular
XX PT activities.
XX PS Claim 12; Fig 4; 636pp; English.
XX CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
XX CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX CC The PRO polynucleotides and polypeptides have cytostatic activity. The
XX CC polynucleotides and polypeptides can be used for detecting the presence
XX CC of PRO polypeptides in samples, for linking bioactive molecules to cells
XX CC and for modulating biological activities of cells, using the polypeptides
XX CC for specific targeting. The polypeptide targeting can be used to kill the
XX CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
XX CC provide specific targeting of bioactive molecules to cells. AAC78600 to
XX CC AAC78987 represent PCR primers and probes used in the isolation of the
XX CC PRO polynucleotide sequences
XX SQ Sequence 492 AA;
Query Match 100.0%; Score 2527; DB 3; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKFPALTYWPLIPLVPLGLTNTAIDPGEQALNKGIAA VKEDAVEMLASGLAYSLMK 60
DB 1 MKKFPALTYWPLIPLVPLGLTNTAIDPGEQALNKGIAA VKEDAVEMLASGLAYSLMK 60
QY 61 FTGPMDSDFKNGVLVFNVNSKRDTRKAVLCMVVAGAI AAVFHTLIAYSDLGYYIINKLHV 120
DB 61 FTGPMDSDFKNGVLVFNVNSKRDTRKAVLCMVVAGAI AAVFHTLIAYSDLGYYIINKLHV 120
QY 121 DESVGSKTRAFILYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQWVFAILL 180
DB 121 DESVGSKTRAFILYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQWVFAILL 180
QY 181 HSHLECREPLLIPLSLYMGALVRCCTTLCGLGYYKNIHDIIPDRSGPELGGDATIRKMLSF 240

DB 181 HSHLECREPLLIPLSLYMGALVRCCTTLCGLGYYKNIHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WWPLALILATQRI SRPIVNL FVSRDLGGSSAA TEAVAILTATY PVGHMPYGLWTEIRAYV 300
DB 241 WWPLALILATQRI SRPIVNL FVSRDLGGSSAA TEAVAILTATY PVGHMPYGLWTEIRAYV 300
QY 301 PAFDKNPNKLVSTNTVTAAHIKFTFVCWALS LTLCTCFVMPFTN VSEKILIDIIGVD 360
DB 301 PAFDKNPNKLVSTNTVTAAHIKFTFVCWALS LTLCTCFVMPFTN VSEKILIDIIGVD 360
QY 361 FAFAELCVVP LRI FSPFPVPTVRAH L TGMLW LTKKTFVLAPSSVLRII VLIALSLVLPY 420
DB 361 FAFAELCVVP LRI FSPFPVPTVRAH L TGMLW LTKKTFVLAPSSVLRII VLIALSLVLPY 420
QY 421 LGVHGATLGVGSL LAGFVGES TWAI AACYVVRKQKKOMENESAT EGEDSAMTDMPTTEE 480
DB 421 LGVHGATLGVGSL LAGFVGES TWAI AACYVVRKQKKOMENESAT EGEDSAMTDMPTTEE 480
QY 481 VTDIVEMRENE 492
DB 481 VTDIVEMRENE 492
RESULT 3
AAU86135
ID AAU86135 standard; protein; 492 AA.
XX AC AAU86135;
XX DT 15-JUL-2002 (first entry)
XX DE Human PRO274 polypeptide.
XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
KW neuroprotective.
XX OS Homo sapiens.
XX FN WO200153486-A1.
XX PD 26-JUL-2001.
XX PF 11-FEB-2000; 2000WO-US003565.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 11-MAR-1999; 99US-0123972P.
XX PR 11-MAY-1999; 99US-0133459P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 22-JUN-1999; 99US-0140650P.
XX PR 22-JUN-1999; 99US-0140653P.
XX PR 20-JUL-1999; 99US-014758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 17-AUG-1999; 99US-0149395P.
XX PR 31-AUG-1999; 99US-0151689P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 05-JAN-2000; 2000WO-US000219.
XX (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
XX PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
XX PI Watanabe CK, Wood WI;
XX DR WPI; 2002-205567/26.
XX DR N-PSDB; ABK40261.

PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 61; Fig 16; 302pp; English.

CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention
XX
SQ Sequence 492 AA;

Query Match 100.0%; Score 2527; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVKFPALTHYWPILRFLVPLGIIITNIAIDFGEQALNRGIAAVKEDAVEMLASGLAYSLMK 60
DB 1 MVKFPALTHYWPILRFLVPLGIIITNIAIDFGEQALNRGIAAVKEDAVEMLASGLAYSLMK 60

QY 61 FFTGPMDSDFKNGVLGVFVNSKRDRTKAVLCMVVAGIAAIVFHTLIAYSDILGYIINKLHV 120
DB 61 FFTGPMDSDFKNGVLGVFVNSKRDRTKAVLCMVVAGIAAIVFHTLIAYSDILGYIINKLHV 120

QY 121 DESVGSKTRAFLYLAAPPFFMDAMANTHAGILLKHKYSLVGCASISDVIAQVVFVAILL 180
DB 121 DESVGSKTRAFLYLAAPPFFMDAMANTHAGILLKHKYSLVGCASISDVIAQVVFVAILL 180

QY 181 HSHLECPRLPIPLSLYMGALVRCCTTLCIGYKXNIHDIIPDRSGPGLGSDATIRKWLSP 240
DB 181 HSHLECPRLPIPLSLYMGALVRCCTTLCIGYKXNIHDIIPDRSGPGLGSDATIRKWLSP 240

QY 241 WPLALILATORISRPVNLVFSRDLGSSAATEAVAILTATVPVGHMPYGLWTEIRAVY 300
DB 241 WPLALILATORISRPVNLVFSRDLGSSAATEAVAILTATVPVGHMPYGLWTEIRAVY 300

QY 301 PAFKNNPSKLVSTSNVTAAHKKFTFCVMAISLTLFCVFWTPNVSEKILIDIIGVD 360
DB 301 PAFKNNPSKLVSTSNVTAAHKKFTFCVMAISLTLFCVFWTPNVSEKILIDIIGVD 360

QY 361 FAPAEFCVPLRIFSEFPVPTVRAHLTGWMTLTKTFVLAPSSVLRIIVLIASLVLPY 420
DB 361 FAPAEFCVPLRIFSEFPVPTVRAHLTGWMTLTKTFVLAPSSVLRIIVLIASLVLPY 420

QY 421 LGVHGATLGVSLLAGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEE 480
DB 421 LGVHGATLGVSLLAGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEE 480

QY 481 VTDIVEMRENE 492
DB 481 VTDIVEMRENE 492

RESULT 4
ASO25188
ID ABO25188 standard; protein; 492 AA.
XX
XX ABO25188;
AC ABO25188;
DT 09-SEP-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO274.
DE Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW cell death; growth induction cascade; blood coagulation cascade;
KW viral infection.
XX

OS Homo sapiens.
XX US2003050239-A1.
PN
XX
PD 13-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00978191.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078910P.
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PR 25-MAR-1998; 98US-0079294P.
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PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
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PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
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PR 09-APR-1998; 98US-0081195P.
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PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
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PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 28-APR-1998; 98US-0083336P.
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PR 25-MAY-2001; 2001US-00817092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00817800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
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PR 29-JUN-2001; 2001US-00821066.
PR 03-JUL-2001; 2001US-00821735.
PR 30-JUL-2001; 2001US-00918595.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Rotstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 2527; DB 6; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 DESVGSKTRRAFLYLAAPFPMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
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Qy 181 HSHLECREPLIPILSLYNGALVRCITICLYGKYNHDIIPDRSGPELGGATIRKMLSF 240
Db 181 HSHLECREPLIPILSLYNGALVRCITICLYGKYNHDIIPDRSGPELGGATIRKMLSF 240
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Qy 361 FAFAECLVVPVLRIFGFFPVPTVRAHLTGWLMTLKKTEVLPAPSSVLRITVLIASLVLPY 420
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Db 361 FAFELCVVPLRIFSFPPVTVRAHLTGWLTKKTFVLAPSSVLRIVLIASIVLPL 420

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Db 421 LGVHGATLGVSLLAGFVCESTWVAIAACYVYRKOKKXKXENESATEGEDSANTDPPTEE 480

QY 481 VTDIVEMREENE 492

Db 481 VTDIVEMREENE 492

RESULT 5

ABU72194

ID ABU72194 standard; protein; 492 AA.

XX AC ABU72194;

XX DT 16-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO274.

XX DE Human; secreted and transmembrane protein; PRO; antiinflammatory;

KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;

KW antidiabetic; gene therapy; inflammatory disease; organ failure;

KW atherosclerosis; cardiac injury; infertility; birth defect;

KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;

KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;

KW tissue typing.

XX OS Homo sapiens.

XX PN US2002192706-A1.

XX PD 19-DEC-2002.

XX PF 24-OCT-2001; 2001US-00999832.

XX PR 17-OCT-1997; 97US-0062250P.

PR 13-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 12-MAR-1998; 98US-0077649P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-0080402P.

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PR 25-MAR-1998; 98US-0078939P.

PR 26-MAR-1998; 98US-0079294P.

PR 27-MAR-1998; 98US-0079663P.

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PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.

PR 01-APR-1998; 98US-0080334P.

PR 08-APR-1998; 98US-0081049P.

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PR 09-APR-1998; 98US-0081195P.

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PR 09-APR-1998; 98US-0081229P.

PR 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081819P.

PR 15-APR-1998; 98US-0081838P.

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PR 22-APR-1998; 98US-0082700P.

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PR 22-APR-1998; 98US-0082804P.

PR 23-APR-1998; 98US-0082796P.

PR 07-OCT-1998; 98WO-US021141.

PR 20-NOV-1998; 98WO-US024855.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 24-AUG-2000; 2000WO-US023328.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 22-MAR-2001; 2001WO-US009552.

PR 25-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021086.

PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Ashtenazi AJ, Baker KP, Botstein D, Desnuyers L, Eaton DL;
Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Klajavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Stewart TA, Tumas D, Williams PM, Wood WI;

WPI; 2003-328860/31.
N-PSDB; ACA63463.

New secreted and transmembrane nucleic acids and polypeptides, designated
as PRO, useful for treating inflammation, organ failure, atherosclerosis,
cardiac injury, infertility, birth defects, premature aging, AIDS, or
cancer.

Claim 12; Fig 4; 453pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which
is at least 80 % sequence identity to, or the full-length coding sequence

CC	of, any of 118 300-2100 nucleotide sequences, which encodes its	
CC	corresponding PRO polypeptide selected from 118 100-700 amino acid	
CC	sequences, all given in the specification. The nucleic acids and	
CC	polypeptides are useful for treating inflammatory diseases, organ	
CC	failure, atherosclerosis, cardiac injury, infertility, birth defects,	
CC	premature aging, AIDS, cancer, or diabetic complications. The nucleic	
CC	acids are useful as hybridisation probes, in chromosome and gene mapping,	
CC	and in generating antisense RNA or DNA. The polypeptides are useful as	
CC	pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful	
CC	in tissue typing. This is the amino acid sequence of a novel human	
CC	secreted and transmembrane PRO polypeptide	
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Qy	1 MVKFPALTHWPLRFLRFLVPLGITNIAIDFGEOALNRGIAAVKEDAVEMLASGLAYSLMK 60	
Db	1 MVKFPALTHWPLRFLRFLVPLGITNIAIDFGEOALNRGIAAVKEDAVEMLASGLAYSLMK 60	
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Qy	121 DESVGSKTRRAFLYLAAPPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180	
Db	121 DESVGSKTRRAFLYLAAPPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180	
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Qy	301 PAFDKNPNKLVSTNTVTAHKKFTFVCWALSLTLCFVWFVTPNVSEKILIDIGVD 360	
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ID	ABU84874 standard; protein; 492 AA.	
XX	AC ABU84874;	
XX	12-AUG-2003 (first entry)	
DT	Human secreted and transmembrane polypeptide PRO274.	
DE	Human; thrombolytic agent; interferon; interleukin; cytokine;	
XX	erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;	
KW	apoptosis related condition; AIDS; amyotrophic lateral sclerosis;	
KW	inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;	
KW	gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;	
KW	hypertension; myocardial ischaemia; kidney disease; carcinogenesis;	
KW	glomerulonephritis; lung disease; pulmonary hypertension; pre-eclampsia;	
KW	bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;	

KW	inflammatory bowel disease; reproductive disorder; premature labour.	
XX	Homo sapiens.	
XX	US2002177553-A1.	
XX	28-NOV-2002.	
PF	15-OCT-2001; 2001US-00978192.	
XX	17-OCT-1997; 97US-0062250P.	
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PR	11-MAR-1998; 98US-0077649P.	
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PR 20-MAR-1998; 98US-0078939P.
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PR 07-OCT-1998; 98US-0021141.
PR 02-NOV-1998; 98US-00184216.
PR 08-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-00202054.
PR 27-DEC-1998; 98US-00218517.
PR 03-JAN-1999; 99US-00000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99US-00005028.
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PR 11-FEB-2000; 2000US-0003565.
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PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-0009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-0017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00871780.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.

PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-00211735.
PR 30-JUL-2001; 2001US-00918585.
XX (GETH) GENENTECH INC.
XX Askenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D,
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,
PI Goddard A, Godowski P, Grimaldi JC, Gurney AL, Hillan KJ, Shelton DL,
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Stewart TA,
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR N-PSDB; ABX92267.
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX Claim 12; Fig 4; 459pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, and for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule may be a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. AB061071-AB061164 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdsIDEntry.html
XX Sequence 492 AA;
SQ Query Match 100.0%; Score 2527; DB 6; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVKFPALTHYWLIRFLVPLGTTITAIIDFGQALNRGIAAVKEDAVEMLASVGLAYSLMK 60
DB 1 MVKFPALTHYWLIRFLVPLGTTITAIIDFGQALNRGIAAVKEDAVEMLASVGLAYSLMK 60
QY 61 FFTGMSDFKNVGLVFNVSKRDRTRKAVLCWVAGAAVFTHTLIAYSDLYGYYINKLHHV 120
DB 61 FFTGMSDFKNVGLVFNVSKRDRTRKAVLCWVAGAAVFTHTLIAYSDLYGYYINKLHHV 120
QY 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAIL 180
DB 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAIL 180
QY 181 HSHLECREPLIPILSLYMGALVRCITLCLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
DB 181 HSHLECREPLIPILSLYMGALVRCITLCLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WNPALILATQIRISRPVNLFSRDLGGSSAATEAVAILTATPYGHPYGLMTIRAVY 300
DB 241 WNPALILATQIRISRPVNLFSRDLGGSSAATEAVAILTATPYGHPYGLMTIRAVY 300
QY 301 PAFDKNPNKLVSTNTVTAAHIKKFTVCMALSLTLCFVNFMTPNVSEKILIDIIIGVD 360
DB 301 PAFDKNPNKLVSTNTVTAAHIKKFTVCMALSLTLCFVNFMTPNVSEKILIDIIIGVD 360

QY 361 FAFACLCVPLRIRSFPPVTVRAHLTGWMLTKFTVLPAPSVLRIRIIVLIASLVLPY 420
 DB 361 FAFACLCVPLRIRSFPPVTVRAHLTGWMLTKFTVLPAPSVLRIRIIVLIASLVLPY 420
 QY 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRQKKWENESATEGEDSANTDMPPTTEE 480
 DB 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRQKKWENESATEGEDSANTDMPPTTEE 480
 QY 481 VTDIVEMRENE 492
 DB 481 VTDIVEMRENE 492

RESULT 8
 ID ABU80341 standard; protein; 492 AA.
 XX AC ABU80341;
 XX DT 24-JUN-2003 (first entry)
 XX DE Human secreted/transmembrane protein PRO274.
 XX KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
 KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
 KW inflammatory disease; necrosis; atherosclerosis; infertility;
 KW premature aging; psoriasis; inflammatory disease; renal disease;
 KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
 KW multiple sclerosis; gene therapy.
 XX OS Homo sapiens.
 XX PN US2003004102-A1.
 XX PD 02-JAN-2003.
 XX PF 15-OCT-2001; 2001US-00978189.
 XX PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 11-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 13-MAR-1998; 98US-0077791P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-007886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 26-JUN-1998; 98US-00105413.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98US-0021141.
 PR 02-NOV-1998; 98US-00184216.
 PR 06-NOV-1998; 98US-00187368.
 PR 20-NOV-1998; 98US-00204855.
 PR 07-DEC-1998; 98US-00202054.
 PR 25-DEC-1998; 98US-00218517.
 PR 03-JAN-1999; 99US-0000106.
 PR 03-MAR-1999; 99US-00254465.

08-MAR-1999; 99US-0005028.
 10-MAR-1999; 99US-0025686.
 10-MAR-1999; 99US-0005159.
 12-MAR-1999; 99US-00267213.
 12-APR-1999; 99US-00284291.
 14-MAY-1999; 99US-00311832.
 14-MAY-1999; 99US-00310733.
 22-JUN-1999; 99US-0012252.
 25-AUG-1999; 99US-00380137.
 25-AUG-1999; 99US-00380138.
 25-AUG-1999; 99US-00380142.
 25-AUG-1999; 99US-00380143.
 30-NOV-1999; 99US-0028313.
 02-DEC-1999; 99US-0028551.
 02-DEC-1999; 99US-0028565.
 16-DEC-1999; 99US-0030095.
 30-DEC-1999; 99US-0031243.
 30-DEC-1999; 99US-0031274.
 05-JAN-2000; 2000US-0000219.
 06-JAN-2000; 2000US-0000277.
 06-JAN-2000; 2000US-0000376.
 11-FEB-2000; 2000US-0003565.
 18-FEB-2000; 2000US-0004341.
 24-FEB-2000; 2000US-0005004.
 01-MAR-2000; 2000US-0005601.
 02-MAR-2000; 2000US-0005841.
 10-MAR-2000; 2000US-0006319.
 21-MAR-2000; 2000US-0007532.
 30-MAR-2000; 2000US-0008439.
 17-MAY-2000; 2000US-0013705.
 22-MAY-2000; 2000US-0014042.
 30-MAY-2000; 2000US-0014941.
 02-JUN-2000; 2000US-0015264.
 28-JUL-2000; 2000US-0020710.
 24-AUG-2000; 2000US-0023328.
 08-NOV-2000; 2000US-0079238.
 10-NOV-2000; 2000US-0030873.
 27-NOV-2000; 2000US-00723749.
 01-DEC-2000; 2000US-0032678.
 20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000US-0034956.
 28-FEB-2001; 2001US-00006520.
 22-MAR-2001; 2001US-00816744.
 22-MAR-2001; 2001US-00816920.
 22-MAR-2001; 2001US-00809552.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00854280.
 25-MAY-2001; 2001US-00817092.
 01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001US-00817800.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001US-0019692.
 29-JUN-2001; 2001US-0021066.
 09-JUL-2001; 2001US-0021735.
 30-JUL-2001; 2001US-00918585.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Borstein D, Deanoyers L, Eaton DL;
 Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME;
 Goddard A, Godowski Fu, Grimaldi JC, Gurney AL, Hillan KJ;
 Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 WPI; 2003-341189/32.
 N-PSDB; ACA66008.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Claim 12; Fig 4; 460pp; English.

PS The invention relates to a new isolated nucleic acid molecule comprising a
XX sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory diseases, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence represents a PRO polypeptide
XX SQ Sequence 492 AA;

Query Match 100.0%; Score 2527; DB 6; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVKPPALTYHPLIRFLVPLGITNIAIDFGQALNRGIAA VKEDAVEMLASYGSLMSK 60
DB 1 MVKPPALTYHPLIRFLVPLGITNIAIDFGQALNRGIAA VKEDAVEMLASYGSLMSK 60
QY 61 FFTGPMDSDFKNGVLFVNSKEDRTKAVLCMVVAGIAA VHTLAYS DGLGYIINKLHV 120
DB 61 FFTGPMDSDFKNGVLFVNSKEDRTKAVLCMVVAGIAA VHTLAYS DGLGYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
DB 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
QY 181 HSHLECREPLIPILSLYMGALVRCCTCLGYIYNKHIDIPDRSGPELGDAIRKMLSF 240
DB 181 HSHLECREPLIPILSLYMGALVRCCTCLGYIYNKHIDIPDRSGPELGDAIRKMLSF 240
QY 241 WPLALILATORISRPINLVFSDRLGSSAATEAVAILTATYVGHMPYGLTEIRAVY 300
DB 241 WPLALILATORISRPINLVFSDRLGSSAATEAVAILTATYVGHMPYGLTEIRAVY 300
QY 301 PAFDKNPSNKLSTNTVTAHIIKFTFVCMALSLTLCFVMTWPNVSEKILIDIIGVD 360
DB 301 PAFDKNPSNKLSTNTVTAHIIKFTFVCMALSLTLCFVMTWPNVSEKILIDIIGVD 360
QY 361 PAFALCVLPRIISFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRIIVLIASLVLPY 420
DB 361 PAFALCVLPRIISFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRIIVLIASLVLPY 420
QY 421 LGVHGATLGVGSLLAGFVGESTVMAIAACYVYRKQKKMENESATEGDSATMDMPTEE 480
DB 421 LGVHGATLGVGSLLAGFVGESTVMAIAACYVYRKQKKMENESATEGDSATMDMPTEE 480
QY 481 VTDIVEMEENE 492

Db 481 VTDIVEMEENE 492

|||||

RESULT 9
ADA24546
ID ADA24546 standard; protein; 492 AA.

XX AC ADA24546;

XX DT 20-NOV-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO274.

XX KW Human; secreted and transmembrane protein; PRO; tissue typing;
XX KW chromosome identification; vaccine; cancer; retinal disorder;
XX KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
XX KW wound healing; Obesity; diabetes; hearing loss; nervous system disorder;
XX KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
XX KW haemoglobin associated disorder.

XX OS Homo sapiens.

XX PN US2003050241-A1.

XX PD 13-MAR-2003.

XX PF 16-OCT-2001; 2001US-00978564.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 03-NOV-1997; 97US-0064249P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 21-NOV-1997; 97US-0066364P.

XX PR 10-MAR-1998; 98US-0077450P.

XX PR 11-MAR-1998; 98US-0077632P.

XX PR 11-MAR-1998; 98US-0077641P.

XX PR 12-MAR-1998; 98US-0077791P.

XX PR 13-MAR-1998; 98US-0078004P.

XX PR 20-MAR-1998; 98US-0078886P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 20-MAR-1998; 98US-0078936P.

XX PR 25-MAR-1998; 98US-0079294P.

XX PR 26-MAR-1998; 98US-0079656P.

XX PR 27-MAR-1998; 98US-0079663P.

XX PR 27-MAR-1998; 98US-0079664P.

XX PR 27-MAR-1998; 98US-0079728P.

XX PR 27-MAR-1998; 98US-0079786P.

XX PR 30-MAR-1998; 98US-0079920P.

XX PR 31-MAR-1998; 98US-0080105P.

XX PR 31-MAR-1998; 98US-0080107P.

XX PR 31-MAR-1998; 98US-0080165P.

XX PR 01-APR-1998; 98US-0080194P.

XX PR 01-APR-1998; 98US-0080327P.

XX PR 01-APR-1998; 98US-0080328P.

XX PR 01-APR-1998; 98US-0080333P.

XX PR 01-APR-1998; 98US-0080334P.

XX PR 08-APR-1998; 98US-0081049P.

XX PR 08-APR-1998; 98US-0081070P.

XX PR 08-APR-1998; 98US-0081071P.

XX PR 09-APR-1998; 98US-0081195P.

XX PR 09-APR-1998; 98US-0081203P.

XX PR 09-APR-1998; 98US-0081229P.

XX PR 15-APR-1998; 98US-0081817P.

XX PR 15-APR-1998; 98US-0081819P.

XX PR 15-APR-1998; 98US-0081838P.

XX PR 15-APR-1998; 98US-0081952P.

XX PR 15-APR-1998; 98US-0081955P.

XX PR 21-APR-1998; 98US-0082568P.

XX PR 21-APR-1998; 98US-0082569P.

22-APR-1998; 98US-0082700P.
22-APR-1998; 98US-0082704P.
22-APR-1998; 98US-0082797P.
22-APR-1998; 98US-0082804P.
23-APR-1998; 98US-0082796P.
27-APR-1998; 98US-0083336P.
28-APR-1998; 98US-0083322P.
29-APR-1998; 98US-0083392P.
29-APR-1998; 98US-0083495P.
29-APR-1998; 98US-0083496P.
29-APR-1998; 98US-0083499P.
29-APR-1998; 98US-0083500P.
29-APR-1998; 98US-0083545P.
29-APR-1998; 98US-0083554P.
29-APR-1998; 98US-0083558P.
29-APR-1998; 98US-0083559P.
30-APR-1998; 98US-0083742P.
05-MAY-1998; 98US-0084366P.
06-MAY-1998; 98US-0084414P.
06-MAY-1998; 98US-0084414P.
06-MAY-1998; 98US-0084414P.
07-MAY-1998; 98US-0084598P.
07-MAY-1998; 98US-0084600P.
07-MAY-1998; 98US-0084627P.
07-MAY-1998; 98US-0084637P.
07-MAY-1998; 98US-0084639P.
07-MAY-1998; 98US-0084640P.
07-MAY-1998; 98US-0084643P.
13-MAY-1998; 98US-0085323P.
13-MAY-1998; 98US-0085338P.
13-MAY-1998; 98US-0085339P.
15-MAY-1998; 98US-0085573P.
15-MAY-1998; 98US-0085579P.
15-MAY-1998; 98US-0085580P.
15-MAY-1998; 98US-0085582P.
15-MAY-1998; 98US-0085689P.
15-MAY-1998; 98US-0085697P.
15-MAY-1998; 98US-0085700P.
18-MAY-1998; 98US-0086023P.
22-MAY-1998; 98US-0086392P.
22-MAY-1998; 98US-0086414P.
22-MAY-1998; 98US-0086430P.
22-MAY-1998; 98US-0086486P.
22-MAY-1998; 98US-0087098P.
28-MAY-1998; 98US-0087106P.
28-MAY-1998; 98US-0087208P.
28-JUN-1998; 98US-0090863P.
28-JUN-1998; 98US-0091010P.
01-JUL-1998; 98US-0091359P.
30-JUL-1998; 98US-0094651P.
11-SEP-1998; 98US-0100038P.
20-NOV-1998; 98US-010021141.
20-NOV-1998; 98US-0109304P.
20-NOV-1998; 98US-0109304P.
22-DEC-1998; 98US-0113296P.
23-DEC-1998; 98US-0113621P.
08-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US0005028.
10-MAR-1999; 99WO-US0005190.
12-MAR-1999; 99US-0123957P.
29-MAR-1999; 99US-0126773P.
21-APR-1999; 99US-0130232P.
28-APR-1999; 99US-0131022P.
28-APR-1999; 99US-0131445P.
14-MAY-1999; 99US-0134287P.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
16-JUN-1999; 99US-0139557P.
23-JUN-1999; 99US-0141037P.
07-JUL-1999; 99US-0142860P.
26-JUL-1999; 99US-0145698P.
26-JUL-1999; 99US-0146222P.
29-OCT-1999; 99US-0162506P.

30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUN-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US009552.
22-MAR-2001; 2001WO-US017092.
25-MAY-2001; 2001WO-US017800.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.

(GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI KJlavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
DR N-FSDB; ADA24545.
XX
XX
PT New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
PS Claim 12; Fig 4; 46lpp; English.
XX
XX The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

Query Match 100.0%; Score 2527; DB 6; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVKFPALTHYWPILRFLVPLGITTNIADFGQALNRGIAAVKEDAVENLASYGLAYSLMK 60
Dd 1 MVKFPALTHYWPILRFLVPLGITTNIADFGQALNRGIAAVKEDAVENLASYGLAYSLMK 60
QY 61 FFTGMSDFKNVGLVFNVNSKRDRTKAVLCMVVAGIAAVERHTLIAYSDLGYYIINKLHHV 120
Dd 61 FFTGMSDFKNVGLVFNVNSKRDRTKAVLCMVVAGIAAVERHTLIAYSDLGYYIINKLHHV 120

QY	121	DSVSGKTRRAFLYLAAFPFMDAMWATHAGILLKHKYSFLVGCASISDVIAQVVFVAILL	180	PR	27-MAR-1998;	98US-0079728P;
				PR	27-MAR-1998;	98US-0079786P;
Db	121	DSVSGKTRRAFLYLAAFPFMDAMWATHAGILLKHKYSFLVGCASISDVIAQVVFVAILL	180	PR	30-MAR-1998;	98US-0079920P;
				PR	30-MAR-1998;	98US-0079923P;
QY	181	HSLECREPLLIPILSLYMGALVRCITLCLGYVKNYHDIIPDSGGPELGGDATIRKWLSP	240	PR	31-MAR-1998;	98US-0080105P;
				PR	31-MAR-1998;	98US-0080107P;
Db	181	HSLECREPLLIPILSLYMGALVRCITLCLGYVKNYHDIIPDSGGPELGGDATIRKWLSP	240	PR	31-MAR-1998;	98US-0080165P;
				PR	31-MAR-1998;	98US-0080194P;
QY	241	WMLALILATORISRPINLVFSRDLGGSSAAATEAVAILTATVPVGHMPYGMLEIRAVY	300	PR	01-APR-1998;	98US-0080327P;
				PR	01-APR-1998;	98US-0080328P;
Db	241	WMLALILATORISRPINLVFSRDLGGSSAAATEAVAILTATVPVGHMPYGMLEIRAVY	300	PR	01-APR-1998;	98US-0080333P;
				PR	01-APR-1998;	98US-0080334P;
QY	301	PAFDKKNPSKNLYSTNTVTAAHKKFTFCVMALSLTLCFVMEFTWPNVSEKILIDIIIGVD	360	PR	08-APR-1998;	98US-0081049P;
				PR	08-APR-1998;	98US-0081070P;
Db	301	PAFDKKNPSKNLYSTNTVTAAHKKFTFCVMALSLTLCFVMEFTWPNVSEKILIDIIIGVD	360	PR	08-APR-1998;	98US-0081071P;
				PR	09-APR-1998;	98US-0081195P;
QY	361	FAFAELCVVPLRIFSPFPVPTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPY	420	PR	09-APR-1998;	98US-0081203P;
				PR	09-APR-1998;	98US-0081229P;
Db	361	FAFAELCVVPLRIFSPFPVPTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPY	420	PR	15-APR-1998;	98US-0081817P;
				PR	15-APR-1998;	98US-0081819P;
QY	421	LGVHGATLGVGSLLAGFVGSGSTVVAIAACVYVYRKQKKOMENESATGEDSAMTDMPTTEE	480	PR	15-APR-1998;	98US-0081952P;
				PR	15-APR-1998;	98US-0081953P;
Db	421	LGVHGATLGVGSLLAGFVGSGSTVVAIAACVYVYRKQKKOMENESATGEDSAMTDMPTTEE	480	PR	21-APR-1998;	98US-0081955P;
				PR	21-APR-1998;	98US-0082568P;
QY	481	VTDIVENREENE	492	PR	21-APR-1998;	98US-0082569P;
				PR	22-APR-1998;	98US-0082700P;
Db	481	VTDIVENREENE	492	PR	22-APR-1998;	98US-0082704P;
				PR	22-APR-1998;	98US-0082797P;
				PR	22-APR-1998;	98US-0082804P;
				PR	23-APR-1998;	98US-0082796P;
				PR	27-APR-1998;	98US-0083362P;
RESULT 10				PR	28-APR-1998;	98US-0083322P;
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ID	ABOI9643	standard; protein; 492 AA.		PR	29-APR-1998;	98US-0083495P;
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KW	KW	peripheral neuropathy; diabetic peripheral neuropathy;		PR	30-APR-1998;	98US-0083742P;
KW	KW	Adis-associated neuropathy; Charcot-Marie-Tooth disease;		PR	30-APR-1998;	98US-0083742P;
KW	KW	Refsum's disease; Abetalipoproteinemia; Tangier disease;		PR	03-MAY-1998;	98US-0084366P;
KW	KW	Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;		PR	06-MAY-1998;	98US-0084414P;
KW	KW	Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy.		PR	06-MAY-1998;	98US-0084458P;
XX	XX			PR	07-MAY-1998;	98US-0084600P;
OS	OS	Homo sapiens.		PR	07-MAY-1998;	98US-0084627P;
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PN	PN	US2003050240-A1.		PR	07-MAY-1998;	98US-0084639P;
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XX	XX	13-MAR-2003.		PR	07-MAY-1998;	98US-0084643P;
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PF	PF	16-OCT-2001; 2001US-00978403.		PR	13-MAY-1998;	98US-0085338P;
XX	XX			PR	13	

XX 17-OCT-2001; 2001US-00978824.
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XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 17-MAR-1998; 98US-00040220.
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PR 20-MAR-1998; 98US-0078910P.
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PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080155P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
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PR 28-MAY-1998; 98US-0087208P.
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PR 26-JUN-1998; 98US-0090863P.
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PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
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PR 22-DEC-1998; 98US-00218517.
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PR 10-MAR-1999; 99US-00285686.
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PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-00311832.
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PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.

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PR	20-DEC-2000;	2000WO-US034956.	
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PR	22-MAR-2001;	2001US-00816920.	
PR	10-MAY-2001;	2001WO-US009552.	
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XX			
PA	(GETH) GENENTECH INC.		
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XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;		
PI			
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DB	61	FFTGPMSDFKNVGLVFVNSKDR	KAVLCMVVAGAAIAVFTHTLAYS
QY	121	DESVGSKTRRAFLYLAAPFPM	DMAWTHAGILLKHKYSFLVGCASIS
DB	121	DESVGSKTRRAFLYLAAPFPM	DMAWTHAGILLKHKYSFLVGCASIS
QY	181	HSHLECREPLIPI	LSLYMGALVRCCTTLCGLYKNIHDI
DB	181	HSHLECREPLIPI	LSLYMGALVRCCTTLCGLYKNIHDI
QY	241	WNPALIIATQISRP	IVNLFVSRDLGSSAATEAVAILTAT
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QY	301	PAFDKNPSNKLVS	TNSNTVTAHIAHKKFTVCNMAISL
DB	301	PAFDKNPSNKLVS	TNSNTVTAHIAHKKFTVCNMAISL
QY	361	FAFALCVVPLRIF	SEFPVTVRAHLTGWMLTKKTFVLA
DB	361	FAFALCVVPLRIF	SEFPVTVRAHLTGWMLTKKTFVLA
QY	421	LGVHGATIGVGS	LLAGFVGESWTWIAAACVYVRKOK
DB	421	LGVHGATIGVGS	LLAGFVGESWTWIAAACVYVRKOK

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PR	23-APR-1998;	98US-0082796P.	PR	02-JUN-1999;	99WO-US012252.
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PR	15-MAY-1998;	98US-0085583P.	PR	02-JUN-2000;	2000WO-US015264.
PR	15-MAY-1998;	98US-0085700P.	PR	28-JUL-2000;	2000WO-US020710.
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PR	22-MAY-1998;	98US-0086392P.	PR	27-NOV-2000;	2000US-00723749.
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PR	28-MAY-1998;	98US-0087098P.	PR	28-FEB-2001;	2001WO-US006520.
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PR	28-MAY-1998;	98US-0087208P.	PR	22-MAR-2001;	2001US-00818920.
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PR	22-DEC-1998;	98US-00202054.			
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PR	23-DEC-1998;	98US-0113296P.			
PR	23-DEC-1998;	98US-0113621P.			
PR	05-JAN-1999;	99WO-US000106.			
			Query Match 100.0%; Score 2527; DB 6; Length 492;		
			Best Local Similarity 100.0%; Pred. No. 1.4e-285;		
			Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MVKFPALTHYWPILRFLVPLGITNIAIDFGEQALNKGIAAVKEDAVEMLASGYLAYSIMK 60			
Db	1	MVKFPALTHYWPILRFLVPLGITNIAIDFGEQALNKGIAAVKEDAVEMLASGYLAYSIMK 60			
Qy	61	FFTGPMSDFKNVGLVFNYSKRDRTKAVLCMVVAGAAAVFHTLIAXSDLGYYIINKLHV 120			

Db 61 FTGPMSPKNGVLVFNVSKRDRTKAVLCMVVAGAAVPHFTLIAYSOLGYIINKLHHV 120
QY 121 DESVSGKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVSGKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
QY 181 HSHLECRPELLIPILSLYMGALVRCITICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECRPELLIPILSLYMGALVRCITICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WPLALILATQIRISPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYCWLTETIRAVY 300
Db 241 WPLALILATQIRISPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYCWLTETIRAVY 300
QY 301 PAFDKNPSNKLVSNTVTAARHKKFTFCVCAVSLTICFVNFMTNPVSEKILIDIGVD 360
Db 301 PAFDKNPSNKLVSNTVTAARHKKFTFCVCAVSLTICFVNFMTNPVSEKILIDIGVD 360
QY 361 FAFABLCVVPLRIFSEFPVPTVRAHLTGWMLTKKTFVLAPSSVLRILVLIASLVLPY 420
Db 361 FAFABLCVVPLRIFSEFPVPTVRAHLTGWMLTKKTFVLAPSSVLRILVLIASLVLPY 420
QY 421 LGVHGATLGVGSLLAGFVGSESTWVAIAACVYTRKOKKOVENESATEGEDSANTDMPPTEE 480
Db 421 LGVHGATLGVGSLLAGFVGSESTWVAIAACVYTRKOKKOVENESATEGEDSANTDMPPTEE 480
QY 481 VTDIVEMRENE 492
Db 481 VTDIVEMRENE 492
RESULT 13
ADB73513
ID ADB73513 standard; protein; 492 AA.
XX AC ADB73513;
XX DT 04-DEC-2003 (first entry)
XX DE Human PRO polypeptide #2.
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW Chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective.
XX OS Homo sapiens.
XX PN US2003045462-A1.
PD 06-MAR-2003.
PF 16-OCT-2001; 2001US-00978608.
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
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PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
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PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081349P.
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PR 09-APR-1998; 98US-0081229P.
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PR 15-APR-1998; 98US-0081838P.
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PR 21-APR-1998; 98US-0082568P.
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PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
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PR 07-MAY-1998; 98US-0084643P.
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PR 15-MAY-1998; 98US-0085573P.
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PR 28-MAY-1998; 98US-0087038P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.

26-JUN-1998; 98US-00105413.
26-JUN-1998; 98US-0090863P.
26-JUN-1998; 98US-0091010P.
26-JUN-1998; 98US-0091359P.
30-JUL-1998; 98US-0094651P.
11-SEP-1998; 98US-0100038P.
07-OCT-1998; 98US-00168978.
07-OCT-1998; 98US-0021141.
07-OCT-1998; 98US-00184216.
06-NOV-1998; 98US-00187368.
20-NOV-1998; 98US-0109304P.
20-NOV-1998; 98US-0024855.
22-DEC-1998; 98US-00202054.
22-DEC-1998; 98US-00218517.
23-DEC-1998; 98US-0113296P.
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05-JAN-1999; 99US-00000106.
05-JAN-1999; 99US-00254465.
08-MAR-1999; 99US-0005028.
10-MAR-1999; 99US-00265686.
10-MAR-1999; 99US-0005190.
12-MAR-1999; 99US-00267213.
12-MAR-1999; 99US-0123957P.
29-MAR-1999; 99US-0126773P.
12-APR-1999; 99US-00284291.
21-APR-1999; 99US-0130232P.
28-APR-1999; 99US-0131022P.
28-APR-1999; 99US-0131445P.
14-MAY-1999; 99US-00311832.
14-MAY-1999; 99US-0134287P.
14-MAY-1999; 99US-0010733.
02-JUN-1999; 99US-0012252.
16-JUN-1999; 99US-0139557P.
23-JUN-1999; 99US-0141037P.
27-JUL-1999; 99US-0142680P.
26-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0146222P.
25-AUG-1999; 99US-00380137.
25-AUG-1999; 99US-00380138.
25-AUG-1999; 99US-00380142.
29-OCT-1999; 99US-0162506P.
30-NOV-1999; 99US-0028313.
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16-DEC-1999; 99US-0030095.
30-DEC-1999; 99US-0031243.
30-DEC-1999; 99US-0031274.
05-JAN-2000; 2000US-0000219.
06-JAN-2000; 2000US-0000376.
11-FEB-2000; 2000US-00031565.
18-FEB-2000; 2000US-0004341.
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02-MAR-2000; 2000US-0005841.
10-MAR-2000; 2000US-0006319.
21-MAR-2000; 2000US-0007532.
30-MAR-2000; 2000US-0008439.
17-MAY-2000; 2000US-0013705.
22-MAY-2000; 2000US-0014042.
30-MAY-2000; 2000US-0014941.
02-JUN-2000; 2000US-0015264.
28-JUL-2000; 2000US-0020710.
24-AUG-2000; 2000US-0023328.
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27-NOV-2000; 2000US-00723749.
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20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000US-0034956.
28-FEB-2001; 2001US-00006520.
22-MAR-2001; 2001US-00816744.
22-MAR-2001; 2001US-00816920.
22-MAR-2001; 2001US-0089552.
10-MAY-2001; 2001US-00854208.
PR

10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00854280.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001US-00872035.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001US-00886342.
29-JUN-2001; 2001US-00886342.
09-JUL-2001; 2001US-0021735.
30-JUL-2001; 2001US-00918585.
XX (GETH) GENENTECH INC.
XX
XX
Query Match 100.0%; Score 2527; DB 7; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVKFPALTYWPLIRPLVPLGITNIAIDFGEOALNRGIAA VKEDAVEMLASGLAYSLMK 60
DB 1 MVKFPALTYWPLIRPLVPLGITNIAIDFGEOALNRGIAA VKEDAVEMLASGLAYSLMK 60
QY 61 FFTGMSDFKNGVLVFNASKRDRTKAVLCMVVAGIAA VFTHTLIAYSDLGYIINKLHV 120
DB 61 FFTGMSDFKNGVLVFNASKRDRTKAVLCMVVAGIAA VFTHTLIAYSDLGYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVFAILL 180
DB 121 DESVGSKTRRAFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVFAILL 180
QY 181 HSHLECREPLIPILSLYMGALVRCITLCLGYVKNHDIIPDRSGPELGGDATIRKMLSF 240
DB 181 HSHLECREPLIPILSLYMGALVRCITLCLGYVKNHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WWPLALILATORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLTEIRAY 300
DB 241 WWPLALILATORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLTEIRAY 300
QY 301 PAFDKNPNKLVSTNTVTAHKKFTFCVCHALSITLFCVWFVTPNVSEKILIDIGVD 360
DB 301 PAFDKNPNKLVSTNTVTAHKKFTFCVCHALSITLFCVWFVTPNVSEKILIDIGVD 360
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DB 361 FAFAEICVPLRIFFSFPFVTVRAHLTGMLTKKTFVLAPSSVLRIITVLIASLVLPY 420
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DB 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKVNESATESGEDSAMDMPTEE 480
QY 481 VTDIVEMRENE 492
DB 481 VTDIVEMRENE 492
RESULT 14
ADB76229
ID ADB76229 standard; protein; 492 AA.
XX
AC ADB76229;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polypeptide #2.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW Chromosome mapping; Gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective.
XX
OS Homo sapiens.

XX US2003083248-A1.
PN 01-MAY-2003.
XX 16-OCT-2001; 2001US-00978757.
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
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PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
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PR 08-APR-1998; 98US-0081047P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 08-APR-1998; 98US-0081195P.
PR 08-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
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PR 22-APR-1998; 98US-0082704P.
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PR 23-APR-1998; 98US-0082736P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
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PR 05-JAN-2000; 2000US-0000219.
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PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
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PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014042.
PR 28-JUL-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 24-AUG-2000; 2000US-0020710.
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PR 01-DEC-2000; 2000US-0032678.

PR 20-DEC-2000; 2000WC-US034956.
PR 28-FEB-2001; 2001WC-US006520.
PR 22-MAR-2001; 2001WC-US009552.
PR 25-MAY-2001; 2001WC-US017092.
PR 01-JUN-2001; 2001WC-US017800.
PR 20-JUN-2001; 2001WC-US019692.
PR 29-JUN-2001; 2001WC-US021066.
PR 09-JUL-2001; 2001WC-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX (GETH) GENENTECH INC.
PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Gimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-755118/71.
DR N-PSDB; ADB76228.
XX
PT New PRO polypeptides useful for treating peripheral neuropathy,
PT neuropathies associated with systemic disease such as post-polio syndrome
PT or AIDS-associated syndrome.
XX
XX Claim 12; Fig 4; 425pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule may be a
CC toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides
CC are useful for treating neuropathy and neuropathy related diseases such
CC as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
Query Match 100.0%; Score 2527; DB 7; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVKFPALTHWPIRLFLVPLGINTIAIDFGEQALNRGIAAAXKEDAVEMLASGLAYSLMK 60
DB 1 MVKFPALTHWPIRLFLVPLGINTIAIDFGEQALNRGIAAAXKEDAVEMLASGLAYSLMK 60
QY 61 FFTGPMSEDFNVLGVFNVSKRDKTKAVLCMVVAGAAIAAFAVHTLIAYSDLGYYIINKLHV 120
DB 61 FFTGPMSEDFNVLGVFNVSKRDKTKAVLCMVVAGAAIAAFAVHTLIAYSDLGYYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAFPMDAMAWTHAGILLKHKYSFLVGCASIDVIAQVVFVAILL 180
DB 121 DESVGSKTRRAFLYLAAFPMDAMAWTHAGILLKHKYSFLVGCASIDVIAQVVFVAILL 180
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DB 181 HSHLECREPILIPILSYMGALVRCITCLGYYKNTHDIIPDRSGELGSDATIRKWLGF 240
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DB 241 WPLALILATQRIISRPITVNLVFSRDLGGSSAAEAVALTATYPVGHMPYGLWTEIRAVY 300
QY 301 PAFDKNPNKVLSTSTNTAAHKKFTFCVCMALSLTLCFMEFTWNVSEKILIDIIIGVD 360
DB 301 PAFDKNPNKVLSTSTNTAAHKKFTFCVCMALSLTLCFMEFTWNVSEKILIDIIIGVD 360
QY 361 FAFALCVPLRIFSPFPVPTVRAHITGWLMTLTKTFFVLAPSSVLRIIVLIASLVLPY 420
DB 361 FAFALCVPLRIFSPFPVPTVRAHITGWLMTLTKTFFVLAPSSVLRIIVLIASLVLPY 420
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Db 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKMENESATEGDSAMTDMPTTEE 480
QY 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492
RESULT 15
ADC43655
ID ADC43655 standard; protein; 492 AA.
XX AC ADC43655;
XX AC ADC43655;
DT 18-DEC-2003 (first entry)
XX Human secreted/transmembrane protein, PRO274.
XX Human; secreted protein; transmembrane protein; PRO; cytostatic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss.
XX Homo sapiens.
XX US2003054986-A1.
XX 20-MAR-2003.
XX 16-OCT-2001; 2001US-00981915.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 15-MAY-1998;	98US-0085700P.	PR 30-MAR-2000;	2000WO-US008439.
PR 15-MAY-1998;	98US-0085704P.	PR 17-MAY-2000;	2000WO-US013705.
PR 18-MAY-1998;	98US-0086023P.	PR 22-MAY-2000;	2000WO-US014042.
PR 22-MAY-1998;	98US-0086392P.	PR 30-MAY-2000;	2000WO-US014941.
PR 22-MAY-1998;	98US-0086414P.	PR 02-JUN-2000;	2000WO-US015264.
PR 22-MAY-1998;	98US-0086430P.	PR 28-JUL-2000;	2000WO-US020710.
PR 22-MAY-1998;	98US-0086486P.	PR 24-AUG-2000;	2000WO-US023328.
PR 28-MAY-1998;	98US-0087098P.	PR 08-NOV-2000;	2000US-00709238.
PR 28-MAY-1998;	98US-0087106P.	PR 27-NOV-2000;	2000US-00723749.
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PR 26-JUN-1998;	98US-00105411.	PR 20-DEC-2000;	2000US-00747259.
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PR 26-JUN-1998;	98US-0091010P.	PR 28-FEB-2001;	2000WO-US008520.
PR 01-JUL-1998;	98US-0091359P.	PR 22-MAR-2001;	2001US-00816744.
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PR 07-OCT-1998;	98US-00168973.	PR 25-MAY-2001;	2001US-00854280.
PR 07-OCT-1998;	98US-00211141.	PR 01-JUN-2001;	2001WO-US017092.
PR 02-NOV-1998;	98US-00184216.	PR 01-JUN-2001;	2001US-00872035.
PR 06-NOV-1998;	98US-00187368.	PR 05-JUN-2001;	2001WO-US017800.
PR 20-NOV-1998;	98US-01093304P.	PR 14-JUN-2001;	2001US-00874503.
PR 07-DEC-1998;	98US-00202054.	PR 19-JUN-2001;	2001US-00882636.
PR 22-DEC-1998;	98US-00218517.	PR 29-JUN-2001;	2001US-00886342.
PR 22-DEC-1998;	98US-0113296P.	PR 29-JUN-2001;	2001WO-US019692.
PR 23-DEC-1998;	98US-0113621P.	PR 09-JUL-2001;	2001WO-US021066.
PR 05-JAN-1999;	99WO-US000106.	PR 30-JUL-2001;	2001WO-US021735.
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PR 10-MAR-1999;	99US-00265686.	XX	
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Best Local Similarity 100.0%; Pred.No. 1.4e-285;

Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MVKFPALHYWPLIRFLVPLIGITNIAIDFGEQALNRGIAAVKEDAVEMLASGLAYSLMK 60

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Db	61	FTFGMSDFQKNGVLVFNVNSKDRDKAVLCMVVAGATAAFPHLLIAYSDDLGYIINKLHHV	120
Qy	121	DSVSGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCAISDSVIAQVFWAILL	180
Db	121	DSVSGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCAISDSVIAQVFWAILL	180
Qy	181	HSHLCRBPILLIPILUSLYNGVALVRCCTLCLGYQKNIHDIIPDRSGPELGGDATIRKMLSF	240
Db	181	HSHLCRBPILLIPILUSLYNGVALVRCCTLCLGYQKNIHDIIPDRSGPELGGDATIRKMLSF	240
Qy	241	WNPFLALLIATORISRPINVLVFSRDLGSSSAATEAVAILTATVPVGHMPYGMWTEIRAVY	300
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Qy	361	PAFAELCVVPLRIFSGFFVPVTVRAHLTGMLTKKTFFVLAPSSVLRIIVLLIASLVLPY	420
Db	361	PAFAELCVVPLRIFSGFFVPVTVRAHLTGMLTKKTFFVLAPSSVLRIIVLLIASLVLPY	420
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Qy	481	VTDIVEMREENE	492
Db	481	VTDIVEMREENE	492

Search completed: April 22, 2004, 13:56:26
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:55:19 ; Search time 23 Seconds
(without alignments)
1104.347 Million cell updates/sec

US-09-978-188A-7

Title: 2527
Sequence: 1 MVFFPALTHYVPLRLFLVPL.....TDMPPTEVTDIVEMRENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1063	42.1	207	4	US-09-489-847-320
2	812	32.1	162	4	US-09-489-847-160
3	586	23.2	114	4	US-09-489-847-321
4	118.5	4.7	518	4	US-09-134-001C-4744
5	109.5	4.3	610	3	US-08-970-725-2
6	108.5	4.3	361	3	US-09-196-520-6
7	104.5	4.1	610	1	US-08-212-188-2
8	104.5	4.1	610	5	PCT-US95-02708-2
9	104	4.1	536	4	US-09-107-532A-5507
10	103	4.1	631	4	US-09-107-532A-3902
11	103	4.1	1058	2	US-08-687-289A-5
12	103	4.1	1058	4	US-09-435-897-5
13	101.5	4.0	877	4	US-09-543-681A-6388
14	100.5	4.0	413	4	US-09-540-236-3672
15	100	4.0	644	4	US-09-252-991A-21730
16	98.5	3.9	472	4	US-09-934-899-10
17	98.5	3.9	516	4	US-09-252-991A-21329
18	98	3.9	534	4	US-09-328-352-6713
19	98	3.9	619	4	US-09-540-236-2377
20	96.5	3.8	509	4	US-09-252-991A-30864
21	96.5	3.8	528	2	US-08-403-852D-21
22	96.5	3.8	528	3	US-08-510-646B-22
23	96.5	3.8	528	3	US-09-231-818-21
24	96.5	3.8	528	4	US-09-635-359B-21
25	96.5	3.8	808	4	US-09-134-001C-3105
26	96.5	3.8	962	4	US-09-328-352-7942
27	95.5	3.8	3287	2	US-08-477-451-7

28	95	3.8	768	4	US-09-489-039A-12897	Sequence 12897, A
29	94	3.7	450	4	US-09-252-991A-28134	Sequence 28134, A
30	93.5	3.7	350	1	US-07-759-568-3	Sequence 3, Appli
31	93.5	3.7	364	3	US-09-196-520-9	Sequence 9, Appli
32	93.5	3.7	551	4	US-09-615-132A-348	Sequence 348, App
33	93.5	3.7	565	4	US-09-489-039A-8414	Sequence 8414, Ap
34	93	3.7	449	4	US-09-328-352-7512	Sequence 7512, Ap
35	93	3.7	474	4	US-09-489-039A-11844	Sequence 11844, A
36	93	3.7	493	4	US-09-134-001C-3486	Sequence 3486, A
37	93	3.7	1065	4	US-09-252-991A-31637	Sequence 31637, A
38	92.5	3.7	466	4	US-09-489-039A-12781	Sequence 12781, A
39	92.5	3.7	513	4	US-09-489-039A-12877	Sequence 12877, A
40	92	3.6	315	1	US-08-118-270-34	Sequence 34, Appl
41	92	3.6	315	5	PCT-US93-08528-34	Sequence 34, Appl
42	92	3.6	483	4	US-09-134-000C-4234	Sequence 4234, Ap
43	91.5	3.6	318	4	US-09-489-039A-10467	Sequence 10467, A
44	91.5	3.6	350	3	US-08-430-286A-8	Sequence 8, Appli
45	91.5	3.6	451	4	US-09-328-352-7659	Sequence 7659, Ap

ALIGNMENTS

RESULT 1

US-09-489-847-320
; Sequence 320, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 320
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-320

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				Gaps	0;
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Qy	346	PNVSEKILDIIGVDPAFAEL	CVVPIRISFFPVPVTVRAHLTGWLT	TKKTFVLAPSSV	405
Db	61	PNVSEKILDIIGVDPAFAEL	CVVPIRISFFPVPVTVRAHLTGWLT	TKKTFVLAPSSV	120
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Qy	466	EGEDSAMTDMPPTEVTDIVEM	RENE	492	
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; Sequence 160, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
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; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (162)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-160

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Best Local Similarity 100.0%; Pred. No. 9.5e-84;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 392 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 451
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Qy 452 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 492
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RESULT 3
US-09-489-847-321
; Sequence 321, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (162)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-321

Query Match 32.1%; Score 812; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 9.5e-84;
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Qy 332 MALSLTLCTFWMFVTPNVSKILLIIGVDFAFALCWLPIRFPFVPTVRAHLTGWL 391
Db 1 MALSLTLCTFWMFVTPNVSKILLIIGVDFAFALCWLPIRFPFVPTVRAHLTGWL 60

Qy 392 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 451
Db 61 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 120

Qy 452 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 492
Db 121 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 161

RESULT 4
US-09-134-001C-4744
; Sequence 4744, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4744
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4744

Query Match 4.7%; Score 118.5; DB 4; Length 518;
Best Local Similarity 20.0%; Pred. No. 0.00025;
Matches 94; Conservative 77; Mismatches 147; Indels 153; Gaps 22;

Qy 53 GLAYSLAKFTGPMDSDFKAVGLVFNVSKRDRTRKAVLCMVVAGAIAAVFHTLIAYSDIGYY 112
Db 124 GDAITLDPDFKRLDDKNI-----IKIISGLIIVVFFTL--YTHSGFV 165

Qy 113 IINKLHVDES VGSKTRRAFLYLAAPFFMDAMAWTHAGILLKH-----KYSFLVG--CASI 166
Db 166 -----SGGK-----LFESAFGLN-----YHAGLLIIVAIIVIPYTFGGYLA VSI 204

Qy 167 SDVIAQVVFVAILLHSHLECEPILIPILSLYMGALVRCCTTCLGVYKNIHDIIIPDR--SG 225
Db 205 TDFQGVIMLIAM-----VWVFIVAI-----LKLNGWDTHTDAQMKPTN 244

Qy 226 PELGGDATIRMLS-FWVPLALILATORISRP-IVNLFVS-----RDLGSSAAT 273
Db 245 LDLFRTGTVLGI VSLFSWGLGY-----FGQPHIIVRFMSIKSHKLPKARRLG---ISW 295

Qy 274 EAVAILTATVPVGHMPYGNLATE-----TRAVVPAPDKN 306
Db 296 NAVGLLGA-IGVGLTGISFISERHIKLEDPETUFIVMSQILFHPVCGFLLAAILAAMS 354

Qy 307 NPSKLVSTSTNTVT-----AAHIKKFTFV---CMALSITLCFVFWFTPNVSE 350
Db 355 TISSQLLVTSLSLTEDFKYLRGSDKASHQKPEVILGRISLVLLVAIVAITIAMHPN--- 411

Qy 351 KILIDIICVDPAFAELCVPLRIFSPFPVTVRAHLTGMLTLKTKFVLAPSSVLRIRIIV 410

US-09-489-847-160
; Sequence 160, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (162)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-160

Query Match 32.1%; Score 812; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 9.5e-84;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 MALSLTLCTFWMFVTPNVSKILLIIGVDFAFALCWLPIRFPFVPTVRAHLTGWL 391
Db 1 MALSLTLCTFWMFVTPNVSKILLIIGVDFAFALCWLPIRFPFVPTVRAHLTGWL 60

Qy 392 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 451
Db 61 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 120

Qy 452 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 492
Db 121 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 161

RESULT 3
US-09-489-847-321
; Sequence 321, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (162)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-321

Query Match 32.1%; Score 812; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 9.5e-84;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 MALSLTLCTFWMFVTPNVSKILLIIGVDFAFALCWLPIRFPFVPTVRAHLTGWL 391
Db 1 MALSLTLCTFWMFVTPNVSKILLIIGVDFAFALCWLPIRFPFVPTVRAHLTGWL 60

Qy 392 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 451
Db 61 MTLKTLFVLAPSSVLRIRIIVLASVLPYLGVHGATLVGSLLAGFVGSSTNVAIAACV 120

Qy 452 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 492
Db 121 YRKQKKMENESATEGSDSANTDMPTEETVTDIVEMREENE 161

RESULT 4
US-09-134-001C-4744
; Sequence 4744, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4744
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4744

Query Match 4.7%; Score 118.5; DB 4; Length 518;
Best Local Similarity 20.0%; Pred. No. 0.00025;
Matches 94; Conservative 77; Mismatches 147; Indels 153; Gaps 22;

Qy 53 GLAYSLAKFTGPMDSDFKAVGLVFNVSKRDRTRKAVLCMVVAGAIAAVFHTLIAYSDIGYY 112
Db 124 GDAITLDPDFKRLDDKNI-----IKIISGLIIVVFFTL--YTHSGFV 165

Qy 113 IINKLHVDES VGSKTRRAFLYLAAPFFMDAMAWTHAGILLKH-----KYSFLVG--CASI 166
Db 166 -----SGGK-----LFESAFGLN-----YHAGLLIIVAIIVIPYTFGGYLA VSI 204

Qy 167 SDVIAQVVFVAILLHSHLECEPILIPILSLYMGALVRCCTTCLGVYKNIHDIIIPDR--SG 225
Db 205 TDFQGVIMLIAM-----VWVFIVAI-----LKLNGWDTHTDAQMKPTN 244

Qy 226 PELGGDATIRMLS-FWVPLALILATORISRP-IVNLFVS-----RDLGSSAAT 273
Db 245 LDLFRTGTVLGI VSLFSWGLGY-----FGQPHIIVRFMSIKSHKLPKARRLG---ISW 295

Qy 274 EAVAILTATVPVGHMPYGNLATE-----TRAVVPAPDKN 306
Db 296 NAVGLLGA-IGVGLTGISFISERHIKLEDPETUFIVMSQILFHPVCGFLLAAILAAMS 354

Qy 307 NPSKLVSTSTNTVT-----AAHIKKFTFV---CMALSITLCFVFWFTPNVSE 350
Db 355 TISSQLLVTSLSLTEDFKYLRGSDKASHQKPEVILGRISLVLLVAIVAITIAMHPN--- 411

Qy 351 KILIDIICVDPAFAELCVPLRIFSPFPVTVRAHLTGMLTLKTKFVLAPSSVLRIRIIV 410

Db 412 DTILNLVGNWAGGAAPSPVLVLSYWKDUTRAGASG-----MWAGAVV 457
QY 411 LIASLVLPYLGVHGATLGVGSLLAGFVGESTMVAIAACYVYRKQKKMEN 461
Db 458 VIVWISMIKPLATINAFPGMYEIIIPGI-----VSVLITIVSKLTKKPPD 503

RESULT 5
US-08-970-725-2
; Sequence 2, Application US/08970725
; Patent No. 6080542
; GENERAL INFORMATION:
; APPLICANT: Becker, Jeffrey M.
; APPLICANT: Stacy, Gary
; TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,725
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,188
; FILING DATE: 16-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 372.6601P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-970-725-2

Query Match 4.3%; Score 109.5; DB 3; Length 610;
Best Local Similarity 18.9%; Pred. No. 0.0034;
Matches 110; Conservative 93; Mismatches 172; Indels 207; Gaps 29;

QY 7 LTHYVPLRFVLPLGITHIADFGQALNR-----GT-----AAVKE--DAV 46
Db 132 LSNFTFCVTPVGAALIA-----DQFLGRNTIVCSAVIIFIGLILITCTAIPSVIDAG 187
QY 47 ENLASVGLAYSLMKFTFGPMSDFKNVGLV-----FVNSKEDRTKAVLCHVAGAI 96
Db 188 KSMGGFVVSLLIIGLGTGK--SNVSPLMABQLPKIPPVYKTKGSKVIVDPWT--- 242
QY 97 AAVFHTLAYSGLGYIINKLHVDESIGS-----KTRAFLYLAAPFMDAXWT 147
Db 243 -----TSRAYM-IFWTIN-----VGSUSVLAATTSLSTKGFVYAYLLPL----- 281
QY 148 HAGILLKHKYSFLVGCASISDVIAQVFWAILLHSHLECPPLIPILSLYMGALVRCCT 207
Db 282 -----CVFVILPI-----ILAVSKTFTSTLLPPVPSLFV--LVKCSS 317
QY 208 LCLGYKYNHDIIPDRSGPELGGDATIRKMLSFWWPLALILATQIRSPIYNLFSRDLG 267

Db 318 LLL--KTNL-----ISKLNH-----LALLLLERYVKQWDDLFID-ELX 354
QY 268 GSSAATEAVAILTATYVPVGHMYPYGLMTEIRAVYPAFDKNNPSNKLVSNTVTAHI--- 324
Db 355 RALRACKTFLF-----YPIYVVCYQGT-----NNLSIQAGQMOTGNVND 395
QY 325 --KKFTFVCMALSLTLC-----FVMTWTFNVSEKILIDI-IGVDFA----- 362
Db 396 LFQAFDSIALIIFIPICDNIYPLRKYNIPKPIRLITLGFMTATASMIYAAVLOAKIY 455
QY 363 -----FAELCV-----VPLRIFSPFPFVTVRAHLTGWLMTLKKTFVVLAPSV 405
Db 456 QRGPCVANFTDTCVNDISVWIOIPAYVLIAPS---EIFASITG---LEPAFTKAPPSM 508
QY 406 LRII-----VLIASLVLPYLGVHGATLGVGSLLAGFVGESNMVALAAC 450
Db 509 KSIITLFLFTNAFGAIISSICISSTAVANPKLTWMTGTGIAVPIAG-----IMFWVCF 561
QY 451 VYRKQKKMENESATEGEDSAMTMDPPTHEEVTDDIVEMRENE 492
Db 562 HHVDAMEDEQNQLEFKRND-ALTKKDVEKVEHDSYMADESQ 602

RESULT 6
US-09-196-520-6
; Sequence 6, Application US/09196520
; Patent No. 6204039
; GENERAL INFORMATION:
; APPLICANT: Falco, Carl S.
; APPLICANT: Allen, Stephen M.
; TITLE OF INVENTION: Plant Isocitrate Dehydrogenase Homologs
; FILE REFERENCE: BB-1291
; CURRENT APPLICATION NUMBER: US/09/196,520
; CURRENT FILING DATE: 1998-11-19
; EARLIER APPLICATION NUMBER: 60/067,388
; EARLIER FILING DATE: December 2, 1997
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (68)
US-09-196-520-6

Query Match 4.3%; Score 108.5; DB 3; Length 361;
Best Local Similarity 21.4%; Pred. No. 0.0019;
Matches 63; Conservative 49; Mismatches 86; Indels 97; Gaps 15;

QY 30 GEQALNRGIAAVKEDAVEMLASVGLAYSLMKFTFGPMSDFKNVGLVFNKEDRTKAVLC 89
Db 105 GHRSLN--LTLRKE--LNLVYVRPCYSL-----PGYKTRYDNVNLITI---RENTG--- 150
QY 90 MVVAGALAAVFTLIAYSGLGYIINKLHHVDESIGSKTRRAFLVLAAPFMDAMAWTHA 149
Db 151 -----FYSGLEHQV--RGVVESLKITRQASLRVAEYAFYAKAHGRE 192
QY 150 GILLKHKYS-----FLVGCASISDVIAQVFWVAILLHS--HLECPPLIPII---S 196
Db 193 RVSAIHKANIMQKTDLGLFKLCCREVAEKYPEITYEBEWDNCCMLVKNPALFDVLWPN 252
QY 197 LYMGALVRCCTTLCGYI-----KNHIDIIPDRSGPELGGDATIRKM 237
Db 253 LY-GDII--SDLCAGLVGGLGTTPSNCIGEGGIALAEVHGAPDIAGKNLAN----- 302
QY 238 LSFWWPLALILA-----TQIRSRPIVNL-----FVSRDLGGSSAATE 274
Db 303 -----FTALLSGVTMLRHLNLHDKAEQIQOKAILNTIAEGKYRTADLOGSSKTE 352

RESULT 7

```
US-08-212-188-2
; Sequence 2, Application US/08212188
; Patent No. 5689039
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY M.
; APPLICANT: STACEY, GARY
; TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,188
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 7493-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: ATPR2ap
;
US-08-212-188-2
Query Match 4.1%; Score 104.5; DB 1; Length 610;
Best Local Similarity 18.5%; Pred. No. 0.013;
Matches 108; Conservative 96; Mismatches 169; Indels 211; Gaps 28;

Qy 7 LTHVPLRLFLVPLGITNIAIDFGEQALNR-----GI-----AAVKE--DAV 46
Db 132 LSNFTFCWCYTPVGAALIA-----DQFLGRYNTIVCSAVIYFGILLICTAIPSIDAG 187

Qy 47 EMLASYGLAYSLMKFFTPGMSDFKNVGLV-----FVNSKRDRTKAVLCWVAGAI 96
Db 188 KSMGFFVSVLIIIGLTGGIK--SNVSPLMAEQLPKIPPYVTKKNGSKVIVDPVVT--- 242

Qy 97 AAVFHTLIAYSDGLGYIINKLHHVDES VGS-----KTRFAFLYLAAPFMDAMWT 147
Db 243 -----TSRAVY-IFYWTIN-----VGSLSVLATTSLESTKGFVAYLLPL----- 281

Qy 148 HAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLECREPLIIPILSLYMGALVRCCT 207
Db 282 -----CVFVIPLI-----ILAVSKTAFTSTLLPPVPSLFV--LVKCSS 317

Qy 208 LCLGYNNKIHDIIPDRSGPELGGDATIRKMLSFWWPLALILATQRIISRPIVNLVFSRDLG 267
Db 318 LLL--KTNL-----ISKLNH---LALLLLERYVKDQWDDLFID-ELK 354

Qy 268 GSSAATEAVAILTATYPVGHMFYGLWLEIR----- 297
Db 355 RALRACKTFLEF---YPIYWCYQMTNNKISQAGQMTGNVSNDLFQAFDSIALIIFIP 410

Qy 298 ----AVPAPFKNPNPSK-----LVSTNSTVTVAHIK-----KFTFVCMA 333
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Db 411 ICNIIYPLLRKYNIFPKIILRITLGFMTATASMIYAAVLQAIYQRGPCYANFTDTCVS 470
Qy 334 LSLTL-----CFWMFTPNVSEKILIDIGVDFAFACELCWPLRIFSPFPVPVTVRAHLT 388
Db 471 NDISVMIQIPAYVLI-----AFSEIFASITGLEPAFTK-----APPSMKSIIT 513
Qy 389 GNLMTLKKTEVLAPSSVLRIRIIVLIASLVLPYLGVHGATLGVGSLLAGFVGESTMVAIAA 448
Db 514 ALFL-----FTNAFGAILSI--CISTAVNPKLTWMTYGTIAVTAFIAG-----IMFWV 559
Qy 449 CYVYRKQKKXKXENESATEGEDSANTDMPPTPEETVTDIVEMREENE 492
Db 560 CFHHYDAMEDEQQLFQKRD-ALTKKQVKEVHSDYSMADESQ 602

RESULT 8
PCT-US95-02708-2
; Sequence 2, Application PC/TUS9502708
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY M.
; APPLICANT: STACEY, GARY
; TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02708
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 7493-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: ATPR2ap
;
PCT-US95-02708-2
Query Match 4.1%; Score 104.5; DB 5; Length 610;
Best Local Similarity 18.5%; Pred. No. 0.013;
Matches 108; Conservative 96; Mismatches 169; Indels 211; Gaps 28;

Qy 7 LTHVPLRLFLVPLGITNIAIDFGEQALNR-----GI-----AAVKE--DAV 46
Db 132 LSNFTFCWCYTPVGAALIA-----DQFLGRYNTIVCSAVIYFGILLICTAIPSIDAG 187

Qy 47 EMLASYGLAYSLMKFFTPGMSDFKNVGLV-----FVNSKRDRTKAVLCWVAGAI 96
Db 188 KSMGFFVSVLIIIGLTGGIK--SNVSPLMAEQLPKIPPYVTKKNGSKVIVDPVVT--- 242

Qy 97 AAVFHTLIAYSDGLGYIINKLHHVDES VGS-----KTRFAFLYLAAPFMDAMWT 147
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Db 243 -----TSRAYM-IFYWTIN-----VGSLSVLATTSLESTKGFYAYLLPL----- 281
QY 148 HAGILLKHYSFLVGCASISDVIAQVFAVAILLHSHLECREPLILPILSLYMGALVRCCT 207
Db 282 -----CVFVIPLI-----ILAVSKTFTSTLLPPVPSLFV--LVKCSS 317
QY 208 LCLGYKNIHDIIPDRSGPELGDAITRKWLSFWWPLALILATORISRPVNLVFSRDLG 267
Db 318 LLL--KTNL-----ISKLNH---LALLLLERYKQDQDLDLFD-ELK 354
QY 268 GSSAAATEAVAILPATYVGHMPYGMWITEIR----- 297
Db 355 RALRACKTFLF-----YPIYWCYQMTNNKISQAGQWQTNVNSDLFQAFDSIALIIFIP 410
QY 298 -----AYPAPDKNPNK-----LVSTSTVTAHAK-----KFTFVCWA 333
Db 411 ICNIIYPLLRKNIIPKPIRLITLGFMTATASMIYAALVQAKIYORGPCYANFTDTCVS 470
QY 334 LSUTL-----CFYMFWTPNVSEKILIDIIGVDFAFACELCVPLRIFSPFPVTVRAHLT 388
Db 471 NDISVNIQIPAYVLI---AFSEIFASITGLEFAFK-----APPSMKSIIIT 513
QY 389 GWMLTKKTFTVLAPSSVLRIRIIVILASLVLPYLGVHGATLGVCSLLAGFVGESTWVAIAA 448
Db 514 ALFL-----FTNAFGAIIISI--CISSTAVNPKUTWMTYGTIAVTAFTAG-----IMFWV 559
QY 449 CVYVRKQKKWENESAFEGSDSAMTPPTEEVTDIVEMEENE 492
Db 560 CFHYDAMEQNLQLEFRND-ALTKKDVEKEVHDSYSMADESQ 602

RESULT 9

US-09-107-532A-5507
; Sequence 5507, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107/532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5507:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...536
; SEQUENCE DESCRIPTION: SEQ ID NO: 5507:
US-09-107-532A-5507

Query Match 4.1%; Score 104; DB 4; Length 536;
Best Local Similarity 20.3%; Pred. No. 0.032;
Matches 82; Conservative 71; Mismatches 138; Indels 112; Gaps 19;

QY 45 AVEMLASGLAYSLMKFTGP-MSDFKNVGLVFVNSKDRDKAYL---CMVVGAGIAAVF 100
Db 91 ALQWGGGLGLLFAFWIYASPLAHASGGBELIPTKRSLSIAVLVPECMVI----- 143
QY 101 HTLIAYSDLYIINK-----LHHVDESVGSKTERRAFLYLAAPPFMDAMWTHAGILLK 154
Db 144 -----RGYFQGNQEMMPYALSQIVEQV---ARIFMLLATFIIMKMDGDIVTAVTQ 192
QY 155 HKYSPLVGCASIDVIAQVFAVAILLHSHLECREPLILPILSLYMGALVRCCTTLCGLYK 214
Db 193 STFAPIG-----MLASILVLLYFLKGH-----QAYTSAFIH-----YSE 227
QY 215 NIHDIPDRSGPELGDAITRKWLSFWWPLALILATORISRPVNLVFSRDLGSSAAE 274
Db 228 NKINI---ATKELLLD-TVKEAIPF-----IIVGSGVTIFKLVDQFTFMKI--MSASTE 275
QY 275 AVAILTATYVPVGHMPYGMWITEIRAVYPAPDFADKNNPSNKLSTNTVTAHAKKFTFVCNMA 334
Db 276 Y-----SNAQLDLFSIFSANPKLTWVIAL 302
QY 335 SLTCLVFMFWTPNVSEKI-LIDIIGVDFAFACELCVPLRIFSPFPVTVRAHLTGWLM 393
Db 303 ATSIAT--GLPLITEAVTLKDRVGL---AKLTSGNLQLEFSFMPFATFGVMLLAYEL- 355
QY 394 LKKTFTVLAPSSVLRIRIIVILASLVLPYLGVHGATLGVCSLLAG 436
Db 356 --NTLFYTPDSLSGNSVLIQASFVGL-FLGLY---MLVSNMLQG 392

RESULT 10

US-09-107-532A-3902
; Sequence 3902, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107/532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 3902:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 631 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...631
 SEQUENCE DESCRIPTION: SEQ ID NO: 3902:
 US-09-107-532A-3902

Query Match 4.1%; Score 103; DB 4; Length 631;
 Best Local Similarity 20.1%; Pred. No. 0.02;
 Matches 97; Conservative 60; Mismatches 167; Indels 158; Gaps 20;

QY 21 GITNIAIDGEGQALNRGIAVKEDAVEMLASVGL-----AYSLMKP 61
 DB 124 GILNSPIDN-----IAAVFAPTLGLVAGSLGKVLALCTSNLLTTSSTGYIILNA 175
 QY 62 FTGPMDFKXNVGLVFNKSRDKTKAVLCVAVAGATAAFVHTLI-AYSGLGYIINKLHV 120
 DB 176 ADAPFYFLPIFLAYTAAKFNTDFIANVIAAL--VYPTIVSAYSD-----221
 QY 121 DESVSGKTRAFILYLAAPFFDMAMATHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
 DB 222 ----SITLR-FLGMPV-----ILARY-----TSTVIPAILAVVWYLS 252
 QY 181 HSHLECREPI-----LIPILSLYMGALV-RTTICLGYKNIHDIIPDR 223
 DB 253 YIEPKIRKLSHESIRNLLPFTCIIVWFVILLVGPDIADYASQLIAGLYAVNFSPVL 312
 QY 224 SGPELGSDATIRKMLFWMPLALILATORISRPVNLVFSRDLGGSSAATEAVAILTATY 283
 DB 313 SGAVIGGFQVGLVIFGLHGLVPM-TNNLS-----FYGRDTLGPACMTAVAA-----359
 QY 284 PVCHMPYGMWLTETRAYVPADK-NPESNKLVSNTVTA-----AHKKFT 328
 DB 360 -----QAGAVLGFVLTNNKVKSLSLSAFITALFGITEPAVVGVTLYKRPFY 408
 QY 329 FVCMALSLTLCFYMFWTPNVSEKILIDIIGVDFAPALCVPLRIFSPFPVPV-----T 382
 DB 409 IAC-----ICGAIFG-----GVAGA--AGAGALAVATRSILSPFIYIGEGFVWL 450
 QY 383 VRAHLTGWMLTKKTFVLA-----PSSVLRILVLIASLVLPYLGVHGATLGVGSLLA 435
 DB 451 VASYFLAMISSCMLTFLFGYKDIEBESSKDIIVLSTPAAGEIIDJSEVNDPTFASGSLGE 510
 QY 436 GF 437
 DB 511 GF 512

RESULT 11
 US-08-687-289A-5
 Sequence 5, Application US/08687289A
 Patent No. 5981195
 GENERAL INFORMATION:
 APPLICANT: Fuller, Forrest H.
 APPLICANT: Krapcho, Karen J.
 APPLICANT: Hammerland, Lance G.
 TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
 IDENTIFYING COMPOUNDS ACTIVE AT
 METABOTROPIC GLUTAMATE RECEPTORS AND

TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
 TREATMENT OF NEUROLOGICAL DISORDERS
 TITLE OF INVENTION: AND DISEASES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 SUITE: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/687,289A
 FILING DATE: July 25, 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/001,526
 FILING DATE: July 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 220/004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1058 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-687-289A-5

Query Match 4.1%; Score 103; DB 2; Length 1058;
 Best Local Similarity 20.3%; Pred. No. 0.045;
 Matches 75; Conservative 57; Mismatches 155; Indels 82; Gaps 21;

QY 110 GYIINKLHVDSVSGSKTRRAFLYLAAPFFDMAMATHAGILLKHYSFLVGCASISDV 169
 DB 477 GRDIMMLQYTEAN-----RYDYVHVGTW-HGVNLNIDDKIQM--NKSGM 519
 QY 170 IAQVVFVAILLHSHLECREPLIPIUSLYMGALVRCITLCLGYKNIHDIIPDRSGPELG 229
 DB 520 VRSV-----CSEPLKQIKVIRKGEVSCWICTACKEN--EFVQD-----558
 QY 230 GDATIRKMLFWMPLALILATORISRPVNLVFSRDLGGSSAATEAV-AILTATYPVGHM 288
 DB 559 -EFTCRACDLGWNPNAELTGCEPI--PVRYLEWS-DIEGIALTLFAVLGFLTAFLVG--612
 QY 289 PYGWLTEIRAVYPAFDKXNPNSKLVSTNTVTAHKKFTFVCMALSLTLCFV---MFWT 345
 DB 613 -----VFIRK-RNTP---IVKATNR-ELSYLLLFSLLC-CFSSSLFFIGEPQDWT 656
 QY 346 PNVSEKILIDIIGVDFAPALCVV--PLRIFSPFPVPVTVRAHLTGWMLTKKTFVLAPS 403
 DB 657 CRLRQ-----PAGGISFVLCISCLIVKTRNVLVFEAKIPTSFHRKMWGLNLQFLVFL-C 711
 QY 404 SVLRILVLIASLVLPYLGVHG-----ATLGVGSLLA-GFVGSTMTVAIAACYVR 453
 DB 712 TFMQIVICVILWYTAAPPSSYRNQEBEIDEIFITCHEGSLMALGFLIGYTCLLAAICFFFA 771
 QY 454 -KQKKQJEN 461
 DB 772 FKSRKLLEN 780

RESULT 12
US-09-435-897-5
; Sequence 5, Application US/09435897A
; Patent No. 6534289
; GENERAL INFORMATION:
; APPLICANT: FULLER, FORREST H.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: HAMMERLAND, LANCE G.
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE TREATMENT
; TITLE OF INVENTION: OF NEUROLOGICAL DISORDERS AND DISEASES
; FILE REFERENCE: 238/301
; CURRENT APPLICATION NUMBER: US/09/435,897A
; CURRENT FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER: 08/687,289
; EARLIER FILING DATE: 1996-07-25
; EARLIER APPLICATION NUMBER: 60/001,526
; EARLIER FILING DATE: 1995-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1058
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized rat mGluR and human calcium receptor
US-09-435-897-5

Query Match 4.1%; Score 103; DB 4; Length 1058;
Best Local Similarity 20.3%; Pred. No. 0.045;
Matches 75; Conservative 57; Mismatches 155; Indels 82; Gaps 21;
QY 110 GYIINKLHVDESQVSKTRAPFLYLAAPFMDAMATHAGILKHKYSLVGCASISDV 169
DB 477 GRDINMLQYTEAN-----RYDYVHVGTW-HEGVINIDYKIQM--NKSQM 519
QY 170 IAQVVFVAILHSHLECREPLIPILSLYMGALVRCITLCLGYKYNTHDIIPDRSGELG 229
DB 520 VRSV-----CSEPLKQKQIKVIRKEVSCCWNICTACKEN--EFVQD----- 558
QY 230 GDATIRKMLSPWPIALILATORISRTVNLVFSRDLGGSSAATEAV-AITLTATYPVGHM 288
DB 559 -EFTCRACDLGWENAEITGCEPI--PVRYLEWS-DIEGALTUFAVLGIFLFAVLG-- 612
QY 289 PYGWLTEIRAVYPADFKNPNKLVSTNTVTAHKKFTFCVCMALSLTLCFV---MFWT 345
DB 613 -----VFIKF-RNTP--IVKATNR-ELSYLLLSLLC-CFSSSLFFIGEPQDWT 656
QY 346 PNVSEKILIDIGVDFAFAELCVV--PLRIFSPFPVPTVRAHLTGWMLTKKTFVLAPS 403
DB 657 CRLRQ-----PAFGISFVLICISILVKTNRVLLVFEAKIPTSFHRKMWGLNLQFLVFL-C 711
QY 404 SVLRRIIVLIASLVPLVGVHG-----ATLGVGSLLA-GFVGESTWVAIAACVYR 453
DB 712 TFMQIVICVILYTA PSSYRNQLEDEIIPITCHEGSLMALGFLGTYTCLLAICFFPA 771
QY 454 -KQKKMEN 461
DB 772 PKSRKLLEN 780

RESULT 13
US-09-543-681A-6388
; Sequence 6388, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6388
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6388

Query Match 4.0%; Score 101.5; DB 4; Length 677;
Best Local Similarity 20.4%; Pred. No. 0.032;
Matches 100; Conservative 60; Mismatches 143; Indels 187; Gaps 23;
QY 131 AFLYLAAPFMDAMAW-----THAGIL---LKHKYSFLVGCA----- 164
DB 140 AFYFILLFEMMSLASNFWLIADQDDSHAGLLVFFTAHAGSVLIMIAFFLWRESGSLD 199
QY 165 -----SISDVIAQVVFV-----AILHSHLECREPLIPILSLYMGALVRCIT 206
DB 200 FDSFRQLSLSPAMASVVELLGFPGKAKGMLPLHSLW---PKAHPAAPSHASALMSGV 255
QY 207 TILCLGYKYNHDIIPDRSGPELGGDATIRKMLSEFWPLALI-----LATQR 252
DB 256 MVKIGIFGII-----KVGIDLLGAS-----QMWGIVVLAFGAVSVLGVWYALAEHD 303
QY 253 ISR-----PIVNLFVSRDLGGSSAATE-----AVAILPATYFV-----GHPYGVW 292
DB 304 LKRLLAHWHTVENIGIILMGVGVGMVGMATDPVIAALGALLGALYHLNHAHVFKGILLFLGA 363
QY 293 LTEIRAVYPA-PDKNPNKLVSTNTVTAHKKFTFCVCMALS----- 335
DB 364 GAIINQIHTRDMKXGGLAKLM--PYTATA-----FLICMAISALPLPLNGFVSEWYTYQ 416
QY 336 --LTCLCFVMFMPNVSEKILIDIGVDFAFAELCVVPLRIFSF-----PPV 379
DB 417 SLFTWSYDGNFVWRLSGPIAIIMLAITGALAAMCFVYGVSVFCGPRSEQAKAKEVPL 476
QY 380 PTVVRAHLTGWL-----NTLKKTFVLAPS----- 404
DB 477 PMTIANGLLALFCVVLGVGAFAVPIIANIAMSSETSALTVTQAILVPSOAMFSP 536
QY 405 VLRIIVLIASLVPLVGVHG---YLVGHG---ATLGVGSLLA-GFVGESTWVAIAACY----- 450
DB 537 ALTFILLIA-LPLIIFLVLGLKGGQPAFRKGNPWACGVYWEKDMAYVAGGFTQALRSM 595
QY 451 ---VTRKQKK 457
DB 596 FAPLYMRKQ 605

RESULT 14
US-09-540-236-3672
; Sequence 3672, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3672
; LENGTH: 413
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3672

Query Match 4.0%; Score 100.5; DB 4; Length 413;
Best Local Similarity 23.5%; Pred. No. 0.019;
Matches 80; Conservative 49; Mismatches 125; Indels 87; Gaps 20;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:57:59 ; Search time 48 Seconds
(without alignments)
2833.871 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527

Sequence: 1 MVKFPALTHYVPLRFLVPL.....TDMPTTEVTDIVEMRENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2527	100.0	492	9	US-09-978-295A-7
2	2527	100.0	492	9	US-09-978-697-7
3	2527	100.0	492	9	US-09-978-192A-7
4	2527	100.0	492	9	US-09-978-832A-7
5	2527	100.0	492	10	US-09-978-189-7
6	2527	100.0	492	10	US-09-978-608A-7
7	2527	100.0	492	10	US-09-978-585A-7
8	2527	100.0	492	10	US-09-978-191A-7
9	2527	100.0	492	10	US-09-978-403A-7
10	2527	100.0	492	10	US-09-978-564A-7
11	2527	100.0	492	10	US-09-999-833A-7
12	2527	100.0	492	10	US-09-981-915A-7
13	2527	100.0	492	10	US-09-978-824-7
14	2527	100.0	492	10	US-09-518-585A-7
15	2527	100.0	492	10	US-09-978-423A-7

16	2527	100.0	492	10	US-09-978-193A-7
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18	2527	100.0	492	10	US-09-978-757A-7
19	2527	100.0	492	10	US-09-978-187B-7
20	2527	100.0	492	10	US-09-978-643A-7
21	2527	100.0	492	10	US-09-978-375A-7
22	2527	100.0	492	10	US-09-978-298A-7
23	2527	100.0	492	10	US-09-978-188A-7
24	2527	100.0	492	10	US-09-978-681A-7
25	2527	100.0	492	10	US-09-978-194A-7
26	2527	100.0	492	10	US-09-999-829A-7
27	2527	100.0	492	10	US-09-978-299A-7
28	2527	100.0	492	10	US-09-978-544A-7
29	2527	100.0	492	10	US-09-978-665A-7
30	2527	100.0	492	10	US-09-978-802A-7
31	2527	100.0	492	12	US-10-164-749A-7
32	2527	100.0	492	12	US-09-999-831A-7
33	2527	100.0	492	12	US-10-013-917A-7
34	2527	100.0	492	12	US-09-999-834A-7
35	2527	100.0	492	12	US-10-162-521A-7
36	2527	100.0	492	12	US-10-211-858-16
37	2527	100.0	492	12	US-10-145-016A-7
38	2527	100.0	492	12	US-10-145-088A-7
39	2527	100.0	492	12	US-10-145-092A-7
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42	2527	100.0	492	12	US-10-165-353A-7
43	2527	100.0	492	12	US-10-167-600-7
44	2527	100.0	492	12	US-10-170-481A-7
45	2527	100.0	492	12	US-10-172-039A-7

ALIGNMENTS

RESULT 1

US-09-978-295A-7
; Sequence 7, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijav, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

[illegible]

; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2527; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVKPPALTHYPLRFLRPLVPLGTNTIAIDFGQALNRGIAA VKEDAVEMLASYG LAYSIMK 60
Db 1 MVKFPALTHYPLRFLRPLVPLGTNTIAIDFGQALNRGIAA VKEDAVEMLASYG LAYSIMK 60
QY 61 FFTGPMSPFQKVLVFNKSKDRTKAVLCMVVAGIAA VFTLTAYS DLYIINKLHV 120
Db 61 FFTGPMSPFQKVLVFNKSKDRTKAVLCMVVAGIAA VFTLTAYS DLYIINKLHV 120
QY 121 DESVGSKTRRFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVGSKTRRFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
QY 181 HSHLECREPLLPIILSYMGALVRCTTCLGYKYNHDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECREPLLPIILSYMGALVRCTTCLGYKYNHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WPLALILATQISRPIVNLVFSRDLGGSSAATEAVAILTATPYGHPMPYGNLWTEIRAVY 300
Db 241 WPLALILATQISRPIVNLVFSRDLGGSSAATEAVAILTATPYGHPMPYGNLWTEIRAVY 300
QY 301 PAFDKNPNKLVSTNTVTAHKKFTFVCNALSILTCFVNFMTFNVSEKILIDIGVD 360
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RESULT 2
US-09-978-697-7
; Sequence 7, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fillvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR APPLICATION NUMBER: 60/085697

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RESULT 3
US-09-978-192A-7
Sequence 7, Application US/09978192A
Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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RESULT 4

US-09-999-832A-7
; Sequence 7, Application US/09999832A
; Publication NO. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P26301C63
; CURRENT APPLICATION NUMBER: US/09/999,832A

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		Query Match		100.0%; Score 2527; DB 9; Length 492;	
		Best Local Similarity		100.0%; Pred. No. 7e-252;	
		Matches 492; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MVKFPALTHWPLIRLPLVPLIGITNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK	60		
Db	1	MVKFPALTHWPLIRLPLVPLIGITNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK	60		
Qy	61	FTGEMSDFNKVGILVFNYSKRDRTKAVLCMVVAGAAVFEHTLIAYSDLGYYIINKLHV	120		
Db	61	FTGEMSDFNKVGILVFNYSKRDRTKAVLCMVVAGAAVFEHTLIAYSDLGYYIINKLHV	120		
Qy	121	DESVGSTRFAFLYLAAPPFMDAMANTHAGILLKHKYSFLVGCASISDVTAQVFFVAILL	180		
Db	121	DESVGSTRFAFLYLAAPPFMDAMANTHAGILLKHKYSFLVGCASISDVTAQVFFVAILL	180		
Qy	181	HSHLECREPLIPILSYMGALVRCCTLCGLYYKNHDIIPDRSGPELGGDATIRKWLSP	240		
Db	181	HSHLECREPLIPILSYMGALVRCCTLCGLYYKNHDIIPDRSGPELGGDATIRKWLSP	240		
Qy	241	WWPLALILATQIRSRPVLNLFVSRDLGSSAAEAVAILTATVPVGHMPYGMWTEIRAVY	300		
Db	241	WWPLALILATQIRSRPVLNLFVSRDLGSSAAEAVAILTATVPVGHMPYGMWTEIRAVY	300		
Qy	301	PAFDKNNPSNKLVTSTNTVTAAHKKFTFVCMAISLTLCFVMTFNVSSEKILIDIIGVD	360		
Db	301	PAFDKNNPSNKLVTSTNTVTAAHKKFTFVCMAISLTLCFVMTFNVSSEKILIDIIGVD	360		
Qy	361	PAFAELCVPLRIFSFPVPVTVRAHLTGWIMTLKKTFLVLAAPSVLRIIVLIASLVLPY	420		
Db	361	PAFAELCVPLRIFSFPVPVTVRAHLTGWIMTLKKTFLVLAAPSVLRIIVLIASLVLPY	420		
Qy	421	LGVHGATLGVGSLLAGFVGSESTWVAIAACVYRKQKKMENESATEGEDSAMTDMPTTE	480		
Db	421	LGVHGATLGVGSLLAGFVGSESTWVAIAACVYRKQKKMENESATEGEDSAMTDMPTTE	480		
Qy	481	VTDIVEMREENE	492		
Db	481	VTDIVEMREENE	492		

RESULT 5

US-09-978-189-7
; Sequence 7, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nagier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923


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QY 361 FAFELCVPLRIPSPFPVPTVRAHLTGWMLTKKTFVLAPSSVLRIRIIVLIASLVLPY 420
Db 361 FAFELCVPLRIPSPFPVPTVRAHLTGWMLTKKTFVLAPSSVLRIRIIVLIASLVLPY 420
QY 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
Db 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
QY 481 VTDIVEMRENE 492
Db 481 VTDIVEMRENE 492

RESULT 6
US-09-978-608A-7
; Sequence 7, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 7
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-7

Query Match 100.0%; Score 2527; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKFPALHYWPLRFLPLGHTNIAIDFGEOALNRGIAAARKEDAVENMLASGLAYSLMK 60
Db 1 MYKFPALHYWPLRFLPLGHTNIAIDFGEOALNRGIAAARKEDAVENMLASGLAYSLMK 60
QY 61 FTGPMSPDKNGLVFNVRKDRTRKAVLCMVVAGAAVAFHTLIAYSDGLYIINKLHV 120
Db 61 FTGPMSPDKNGLVFNVRKDRTRKAVLCMVVAGAAVAFHTLIAYSDGLYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAFPFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAIL 180
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Db 121 DESVGSKTRRAFLYLAAFPFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAIL 180
QY 181 HSHLECREPLIPILSLYMGALVRCCTTCLGYGYNHDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECREPLIPILSLYMGALVRCCTTCLGYGYNHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WPLALIIATQRIISRPINLVFVSRDLGSSAATAVAAILTATYVGHMFPYGLWTEIRAVY 300
Db 241 WPLALIIATQRIISRPINLVFVSRDLGSSAATAVAAILTATYVGHMFPYGLWTEIRAVY 300
QY 301 PAFDKNPNKLVSTNTVTAHIIKKTFFVCMALSLTLCFVWFMTPNVSEKILIDIIGVD 360
Db 301 PAFDKNPNKLVSTNTVTAHIIKKTFFVCMALSLTLCFVWFMTPNVSEKILIDIIGVD 360
QY 361 FAFELCVPLRIPSPFPVPTVRAHLTGWMLTKKTFVLAPSSVLRIRIIVLIASLVLPY 420
Db 361 FAFELCVPLRIPSPFPVPTVRAHLTGWMLTKKTFVLAPSSVLRIRIIVLIASLVLPY 420
QY 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
Db 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
QY 481 VTDIVEMRENE 492
Db 481 VTDIVEMRENE 492

RESULT 7
US-09-978-585A-7
; Sequence 7, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 7
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-7

Query Match 100.0%; Score 2527; DB 10; Length 492;
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Best Local Similarity 100.0%; Pred. No. 7e-252;			
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	MVKPALTTHYPLRFVPLGITHAIDFGQALNRGIAAVKEDAVEMLASYGGLAYSLMK	60
Qy	61	FFTGPMSDFKNVGLVFVNSKRDRTKAVLCMVVAGAAVHTLLIAYSDLGYYIINKLHHV	120
Db	61	FFTGPMSDFKNVGLVFVNSKRDRTKAVLCMVVAGAAVHTLLIAYSDLGYYIINKLHHV	120
Qy	121	DESVGSKTRRAFLYLAAPFMDMAWTHAGILLKHKYSPINGCASISDVIAQVVFVAILL	180
Db	121	DESVGSKTRRAFLYLAAPFMDMAWTHAGILLKHKYSPINGCASISDVIAQVVFVAILL	180
Qy	181	HSHECREPLIPIILSLYMGALVRCITLCLGYKYNHDIIPDRSGPELGGDATIRKMLSF	240
Db	181	HSHECREPLIPIILSLYMGALVRCITLCLGYKYNHDIIPDRSGPELGGDATIRKMLSF	240
Qy	241	WWPLALIATORISRPVNLVFSRDLGGSSAATENAVAILTATYPVGHMPYGLWTEIRAVY	300
Db	241	WWPLALIATORISRPVNLVFSRDLGGSSAATENAVAILTATYPVGHMPYGLWTEIRAVY	300
Qy	301	PAFDKQNTSNKLVSTNTVTAHKKFTFVCMALSLTLCFVWFMTNPVSEKILIDIIGVD	360
Db	301	PAFDKQNTSNKLVSTNTVTAHKKFTFVCMALSLTLCFVWFMTNPVSEKILIDIIGVD	360
Qy	361	FAFALCVVPLRIPSPFPVPTVRAHLTGWLMTLKKTFVLPAPSSVLRIVLIASLVLPY	420
Db	361	FAFALCVVPLRIPSPFPVPTVRAHLTGWLMTLKKTFVLPAPSSVLRIVLIASLVLPY	420
Qy	421	LGVGATLGVGLLAGFVCESTWVAIAACVYVRKQKKXENESATGEDESDMTDMPFTEE	480
Db	421	LGVGATLGVGLLAGFVCESTWVAIAACVYVRKQKKXENESATGEDESDMTDMPFTEE	480
Qy	481	VTDIVEMREENE 492	
Db	481	VTDIVEMREENE 492	

RESULT 8
US-09-978-191A-7
; Sequence 7, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR FILING DATE: 1998-03-11
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; PRIOR APPLICATION NUMBER: 60/078886
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; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071

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;; PRIOR APPLICATION NUMBER: 60/085697
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Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MVKFPALHYWPLIRFLVPLGITNIAIDFGQALNRGIAAVKEDAVEMLASYGSLAYSLMK 60
QY 61 FETGMSDFKQVGLVFNKEDRTKAVLCMVVAGAAVFTLTAIYSDLYGYYIINKLHV 120
DB 61 FETGMSDFKQVGLVFNKEDRTKAVLCMVVAGAAVFTLTAIYSDLYGYYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAFPMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVALL 180
DB 121 DESVGSKTRRAFLYLAAFPMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVALL 180
QY 181 HSHLECREPLILPILSLYMGALVRCITICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
DB 181 HSHLECREPLILPILSLYMGALVRCITICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WMLALILATORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMFPYGNLTEIRAVY 300
DB 241 WMLALILATORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMFPYGNLTEIRAVY 300
QY 301 PAFDKNPNKLVSTNTVTAAHIKFTFCVWALSLTLCFVWFTPNVSEKILIDIIIGVD 360
DB 301 PAFDKNPNKLVSTNTVTAAHIKFTFCVWALSLTLCFVWFTPNVSEKILIDIIIGVD 360
QY 361 FAFaelCVVPLRIFSPFPVPTVRAHLTGWLMTLTKTFLAPSSVLRIRIIVLASLVLPY 420
DB 361 FAFaelCVVPLRIFSPFPVPTVRAHLTGWLMTLTKTFLAPSSVLRIRIIVLASLVLPY 420
QY 421 LGVHGATLGVGSLLAGFVCESTWVAIAACVYVRKOKKXWENESATEGSDSAMTDMPTTEE 480
DB 421 LGVHGATLGVGSLLAGFVCESTWVAIAACVYVRKOKKXWENESATEGSDSAMTDMPTTEE 480
QY 481 VTDIVEMRENE 492
DB 481 VTDIVEMRENE 492
RESULT 9
US-09-978-403A-7
; Sequence 7, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Query Match	100.0%;	Score 2527;	DB 10;	Length 492;		
Best Local Similarity	100.0%;	Pred. No. 7e-252;				
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61	FTGTGMSDFK	NYGLVFVNS	KRDTKAVL	CMWVAGAIAA	VFHTLIAYS	DLYGYIINKLHHV 120
121	DSVSGKTRR	AFLYAA	FPFMDAM	WTHAGIILL	KHKYSFLV	CASISDVIAQVVFVAILL 180
121	DSVSGKTRR	AFLYAA	FPFMDAM	WTHAGIILL	KHKYSFLV	CASISDVIAQVVFVAILL 180
181	HSHLECREP	LLIPILS	LYNGALV	RCTTCLG	YGYKNIHDI	IPRSGPELGGDATIRKMLSF 240
181	HSHLECREP	LLIPILS	LYNGALV	RCTTCLG	YGYKNIHDI	IPRSGPELGGDATIRKMLSF 240
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301	PAPDKNPNK	LVSTNTV	TAAHIK	PTVCNALS	TLTCFVNFWTPNV	USEKILIDIIGVD 360
361	FAPAEJC	VVPLR	IFSPFP	VPVTRAHL	TGWLTKKT	FVLAPSSVLRILVILIASVLVLPY 420
361	FAPAEJC	VVPLR	IFSPFP	VPVTRAHL	TGWLTKKT	FVLAPSSVLRILVILIASVLVLPY 420
421	LGVHGATL	GVGSLLAG	FVGEST	WVAIAACYVVR	KQKKMENES	ATEGEDSAMTDMPPTEE 480
421	LGVHGATL	GVGSLLAG	FVGEST	WVAIAACYVVR	KQKKMENES	ATEGEDSAMTDMPPTEE 480
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481	VTDIVEM	RENE	492			

RESULT 11

US-09-999-833A-7

Sequence 7, Application US/09999833A

Publication No. US20030054405A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleen

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

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APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

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APPLICANT: Hillan, Kenneth J.

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APPLICANT: Kuo, Sophia S.

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APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079663

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PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081070

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081049

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PlC12
CURRENT APPLICATION NUMBER: US/09/981,915A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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/	PRIOR APPLICATION NUMBER: 60/085697
Query Match 100.0%; Score 2527; DB 10; Length 492;	
Best Local Similarity 100.0%; Pred. No. 7e-253;	
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 MVKFPALTYWFLIRFLVPLGTTNIAIDFGQALNRGIAA VKSDAVEMLASYGLAYSLMK 60
Dd	1 MVKFPALTYWFLIRFLVPLGTTNIAIDFGQALNRGIAA VKSDAVEMLASYGLAYSLMK 60
Qy	61 PFTGPMDSFKANGLVFVNKSDRTKAVLCMWAGAAVAASHHTLIAYSDLGYIINKLHHV 120
Dd	61 PFTGPMDSFKANGLVFVNKSDRTKAVLCMWAGAAVAASHHTLIAYSDLGYIINKLHHV 120
Qy	121 DESVGSKTRRAFLYLAAFFPMDAMAWTHAGILLXHKYSFLVGCAISDVIQAQVFWFVAILL 180
Dd	121 DESVGSKTRRAFLYLAAFFPMDAMAWTHAGILLXHKYSFLVGCAISDVIQAQVFWFVAILL 180
Qy	181 HSHLECREPLLIPILSLYNGALVRCTTILCLGYKNHIHDIIPDRSGPELGDATIRKMLSF 240
Dd	181 HSHLECREPLLIPILSLYNGALVRCTTILCLGYKNHIHDIIPDRSGPELGDATIRKMLSF 240
Qy	241 WFLALILATORISRPNVLFSYRDLGGSSAATEAVAILTATPYVPGHMPYGMTEIRAVY 300

Db	241	WPLALIALIATORISRPVNLVFSRDLGSSNAEVAAILTATYPVGHMPVGMLEIRAVY	300
Qy	301	PAFDKKNPSNKLVSSTNTVTAHHKFTFCVMALSLTLCFVMTWTPNVSEKILIDIIIGVD	360
Db	301	PAFDKKNPSNKLVSSTNTVTAHHKFTFCVMALSLTLCFVMTWTPNVSEKILIDIIIGVD	360
Qy	361	FAPAEICVVPILRIISFRFPVPTVRAHLTGMLTKTFFVLAPSSVLRITVLIASLVLPY	420
Db	361	FAPAEICVVPILRIISFRFPVPTVRAHLTGMLTKTFFVLAPSSVLRITVLIASLVLPY	420
Qy	421	LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKKMNESATGEGSAMDMPPTBE	480
Db	421	LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKKMNESATGEGSAMDMPPTBE	480
Qy	481	VTDIVEMRENE	492
Db	481	VTDIVEMRENE	492
RESULT 13			
US-09-978-824-7			
; Sequence 7, Application US/09978824			
; Publication No. US20030055216A1			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Baker Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleon			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austinn L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Kijavini, Ivar J.			
; APPLICANT: Kuo, Sophia S.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James;			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Shelton, David L.			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P2630P1C14			
; CURRENT APPLICATION NUMBER: US/09/978,824			
; CURRENT FILING DATE: 2001-10-17			
; PRIOR APPLICATION NUMBER: 09/918585			
; PRIOR FILING DATE: 2001-07-30			
; PRIOR APPLICATION NUMBER: 60/062250			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/064249			
; PRIOR FILING DATE: 1997-11-03			
; PRIOR APPLICATION NUMBER: 60/065311			
; PRIOR FILING DATE: 1997-11-13			
; PRIOR APPLICATION NUMBER: 60/066364			
; PRIOR FILING DATE: 1997-11-21			
; PRIOR APPLICATION NUMBER: 60/077450			
; PRIOR FILING DATE: 1998-03-10			
; PRIOR APPLICATION NUMBER: 60/077632			
; PRIOR FILING DATE: 1998-03-11			
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; PRIOR FILING DATE: 1998-03-11			
; PRIOR APPLICATION NUMBER: 60/077649			

[illegible]

Query Match 100.0%; Score 2527; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKFPALHYWPLIRFLVPLGNTIAIDFGEQALNRGIAAVKEDAVEMASYGLAYSLMK 60
DB 1 MYKFPALHYWPLIRFLVPLGNTIAIDFGEQALNRGIAAVKEDAVEMASYGLAYSLMK 60
QY 61 FTGPMDSDFKNGVLVFNKSRDRTKAVLCMWVAGIAA VEHFTLIAYSDLGYYIINKLHV 120
DB 61 FTGPMDSDFKNGVLVFNKSRDRTKAVLCMWVAGIAA VEHFTLIAYSDLGYYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQWVFVAILL 180
DB 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQWVFVAILL 180
QY 181 HSHLECREBLLPIILSLYNGALVRCITCLGYKKNIHDIIPDRSGPELGGDATIRKMLSF 240
DB 181 HSHLECREBLLPIILSLYNGALVRCITCLGYKKNIHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WYPLALILATQIRSRPIVNLFSRDLGGSSAATEAVAILTATYPVGHMPYGMWLTIRAVY 300
DB 241 WYPLALILATQIRSRPIVNLFSRDLGGSSAATEAVAILTATYPVGHMPYGMWLTIRAVY 300
QY 301 PAFDKNPNKLVSTNTTAAHIKFTFVCMALSLTLCFVWFMTNPNVSEKILLIDIIGVD 360
DB 301 PAFDKNPNKLVSTNTTAAHIKFTFVCMALSLTLCFVWFMTNPNVSEKILLIDIIGVD 360
QY 361 FAFAEUCVPLRIFSPFPVTVRAHLTGWLTKTFLVAPSSVLRIVILASLVLPY 420
DB 361 FAFAEUCVPLRIFSPFPVTVRAHLTGWLTKTFLVAPSSVLRIVILASLVLPY 420
QY 421 LGVHGATLGVSLLAGFVGESTWVAIAACYVYRKQKKKNENESATEGEDSAMTDMPTTEE 480
DB 421 LGVHGATLGVSLLAGFVGESTWVAIAACYVYRKQKKKNENESATEGEDSAMTDMPTTEE 480
QY 481 VTDIVEMRENE 492
DB 481 VTDIVEMRENE 492

RESULT 14
US-09-918-585A-7
Sequence 7, Application US/0918585A
Publication No. US2003006046A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deansoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pacini, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 2527; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVKFPALTHYWLIRFLVPLGITNIAIDFGEQALNRGIAA VKEDAVEMLASYLAYS LMK 60
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Db 61 FTTGPMSPDNVGLVFNVRKDRRTXAVLCMVVAGIAA VFFHTLIAYS DLYIINKLHV 120

Qy 121 DESVGSKTRRAFLYLAAPFPMDAMANTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180
Db 121 DESVGSKTRRAFLYLAAPFPMDAMANTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180

Qy 181 HSHLECREPLLIPIILSYNGALVRCCTTICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECREPLLIPIILSYNGALVRCCTTICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240

Qy 241 WNPALILATORISREPIVNLVSRDLGGSSAATEAVAILTATYPVGHMPYGLTEIRAY 300
Db 241 WNPALILATORISREPIVNLVSRDLGGSSAATEAVAILTATYPVGHMPYGLTEIRAY 300

Qy 301 PAFDKNPNKLVSTSTNTVTAHHKFTFCVNMALSLTLCFVNMFWTPNVSEKILIDIIGVD 360
Db 301 PAFDKNPNKLVSTSTNTVTAHHKFTFCVNMALSLTLCFVNMFWTPNVSEKILIDIIGVD 360

Qy 361 PAFDELCVVPLRIEFPFPVTVRAHLTGMLTKKTFVLAAPSSVLRILVILASLVWLPY 420
Db 361 PAFDELCVVPLRIEFPFPVTVRAHLTGMLTKKTFVLAAPSSVLRILVILASLVWLPY 420

Qy 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKMENESATEGEDSAMTDPPTTEE 480
Db 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKMENESATEGEDSAMTDPPTTEE 480

Qy 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492

RESULT 15
US-09-978-423A-7
; Sequence 7, Application US/09978423A
; Publication No. US20030069178A1
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GENERAL INFORMATION:
APPLICANT: Aehkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-06
PRIOR APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
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PRIOR APPLICATION NUMBER: 60/082700
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PRIOR FILING DATE: 1998-04-27
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PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545

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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 2527; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MVKFPALTHYWPFLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGGLAYSLMK 60
Db      1  MVKFPALTHYWPFLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGGLAYSLMK 60

QY      61  FTTGPMSPKNGVLVFNVSQRDRTKAVLCMVVAGIAAVFHTLAYSGLYIIINKLHV 120
Db      61  FTTGPMSPKNGVLVFNVSQRDRTKAVLCMVVAGIAAVFHTLAYSGLYIIINKLHV 120

QY      121  DESVSGKTRAFYLXLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
Db      121  DESVSGKTRAFYLXLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180

QY      181  HSHLECREPLLIPIISLYNGALVRCTTICLGYKXNHDIIPDRSGPELGGDATIRKMLSF 240
Db      181  HSHLECREPLLIPIISLYNGALVRCTTICLGYKXNHDIIPDRSGPELGGDATIRKMLSF 240
```

```

QY      241  WPLALILATORISRPIVNLVFSRDLGGSSAATEAVAILTATYFVGHMPYXGWLTEIRAVY 300
Db      241  WPLALILATORISRPIVNLVFSRDLGGSSAATEAVAILTATYFVGHMPYXGWLTEIRAVY 300

QY      301  PAPDKNPSNKLVSISNTVTRAHIKKFTFVCMAISLTLCTFVMTWTPNVSEKILIDIIIGVD 360
Db      301  PAPDKNPSNKLVSISNTVTRAHIKKFTFVCMAISLTLCTFVMTWTPNVSEKILIDIIIGVD 360

QY      361  FAFaelcVvPlRiFsfFvPvTVRAHlTGWlMTlKtFvLAPSSvLRIiVlIAsLVlPY 420
Db      361  FAFaelcVvPlRiFsfFvPvTVRAHlTGWlMTlKtFvLAPSSvLRIiVlIAsLVlPY 420

QY      421  LGVHGATLGVSLLAGFVGESTMVAIAACYYVRKQKKKXNENESATEGEDSANTDMPETEE 480
Db      421  LGVHGATLGVSLLAGFVGESTMVAIAACYYVRKQKKKXNENESATEGEDSANTDMPETEE 480

QY      481  VTDIVEMEENE 492
Db      481  VTDIVEMEENE 492

Search completed: April 22, 2004, 14:03:55
Job time : 50 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:54:13 ; Search time 20 seconds
(without alignments)
2366.312 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527
Sequence: 1 MVKFPALHYWFLIRFLVPL.....TMDPPTTEVTDIVMRSENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Dir1:*
- 2: Dir2:*
- 3: Dir3:*
- 4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	183.5	7.3	449	2 AE1952	hypothetical prote
2	180.5	7.1	433	2 AH2337	hypothetical prote
3	119.5	4.7	693	2 C81078	carbon starvation
4	117.5	4.6	693	2 B81865	carbon starvation
5	115.5	4.6	670	2 S78182	NADH2 dehydrogenas
6	115	4.6	444	2 AF1121	PTS betagluco-side-
7	115	4.6	507	2 B83988	proline transporte
8	114.5	4.5	447	2 F69433	conserved hypotet
9	113.5	4.5	512	2 B89078	high affinity prol
10	113.5	4.5	586	2 S02154	NADH2 dehydrogenas
11	112.5	4.5	398	2 AD0828	probable transmemb
12	112.5	4.5	497	2 T48676	proline uptake pro
13	111	4.4	622	2 E69609	cytochrome-c oxida
14	110.5	4.4	400	2 AB0967	probable membrane
15	110.5	4.4	452	2 AB1437	PTS system, cellob
16	108.5	4.3	427	2 C82221	conserved hypotet
17	108.5	4.3	450	2 AC1079	PTS system, cellob
18	108.5	4.3	492	2 AC0768	probable transmemb
19	108	4.3	444	2 AI1481	PTS betagluco-side-
20	108	4.3	740	2 AB0600	probable membrane
21	107	4.2	416	2 JT0487	lactose permease -
22	107	4.2	422	1 A69853	hexuronate transpo
23	106	4.2	334	2 A64447	hypothetical prote
24	105.5	4.2	372	2 T48350	3-isopropylmalate
25	105	4.2	404	2 H64175	hypothetical prote
26	105	4.2	561	2 AG3119	ABC transporter, m
27	105	4.2	561	2 H98167	hypothetical prote
28	105	4.2	592	2 H97105	carbon starvation
29	105	4.2	1019	2 B71874	probable cation ef

hypothetical prote
probable amino aci
galactoside permea
galactoside permea
bicyclomycin resis
probable sodium/so
lactose permease -
sodium/proline sym
citrate carrier pr
citrate-sodium sym
hypothetical prote
NADH2 dehydrogenas
probable transport
spoVB related memb
cation efflux syst
citrate carrier pr

ALIGNMENTS

RESULT 1

AE1952
hypothetical protein all1168 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1952
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1952
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <KUR>
A:Cross-references: CB:BA000013; PIDN:BB73125.1; PID:gl7130514; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1168

Query Match	7.3%	Score 183.5;	DB 2;	Length 449;
Best Local Similarity	21.0%	Pred. No. 2.3e-07;		
Matches	97;	Conservative	92;	Mismatches 201;
			Indels	71;
			Gaps	14;
QY	13	LIRFLVPLGINTNIAIDFGE	---	QALNRGIIAAVKEDAVEMLASYGSLAYSLMKFTGPMSD 68
Db	25	LITQFIPLSLSDVANTLGDPLQTSALSR	--	LAFPQ---ETLAGVGVKGVAVFLESPIIM 79
QY	69	PKNVGLVFNVNSKRDRTRAVLCMVVAGIAAVFHTLIAYSDLGYYIINKLHHVDESUGSKT 128		
Db	80	ILHASTALGGQAKSRRLAQWQFTIIAGLVSGIFLLLTWEPYNNLLLDVFGVSSLIQORG 139		
QY	129	RRAFILYLAAPFPMDAMAWTHAGILLKHKYSPLVGCASISDVIAQVWFVAILLHSHLECRE 188		
Db	140	RTAFILMLFVFIWARRFFQGLLIRAKSTAVGASVARLTWVSVLVGVNLRDGM 199		
QY	189	PLILPILSYLNGALVRCITCLGYKKNIHDIIPDRSGP	---	ELGGDATIRKM-----L 238
Db	200	LAGITMGAIIIEAVLVTWFCI	---	RLGAISILEQQGYSETKXLPQTJSGV 247
QY	239	SFWW-PLAILIATQIRSPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLWTEI-		296
Db	248	SFYLPFLASTMLIVGARAILLISLIARSFDGSL	---	ALAVWPAT-----WGLLSIA 296
QY	297	-----RAVPAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVFMFWPNVS		349
Db	297	NGTRMIQQVVISAYEE	---	TSRRTLAAFV-----IIVGLSFTLIPFLGFTDQG 342
QY	350	EKILIDIGVDFAPFABLVCVPLRIFSPFPVTVRAHLTGMLTKKTFVLAPSSVLR--		407
Db	343	LFLLRQFLGNPFLSEASRPVIQLSCFPILLALQNTFQGLLIHKGNWFINLATVVAAT		402

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vi
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: C81078
A:Status: preliminary
A:Superfamily: carbon starvation protein

Query Match 4.7%; Score 119.5; DB 2; Length 693;
Best Local Similarity 22.2%; Pred. No. 0.077;
Matches 111; Conservative 69; Mismatches 181; Indels 139; Gaps 26;
A:Residues: 1-693 <TET>
A:Cross-references: GB:AB002498; GB:AB002098; NID:g7226724; PIDN:AAF41849.1; PID:g72267;
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1493
C:Superfamily: carbon starvation protein

QY 12 PLIRFLPLGINTIAIDFGE-QALNRGTAAYKEDAVEMLASYGSLAYSLMKFTGPMSPDK 70
DB 270 PVMLLTTPRDVLTSTPKIGTIAALGIVIV-NPALQMPAVTHFDGSGPVFSGALPFF- 327
QY 71 NVGLVFNKRDRTKAVLCMVVAGAAVAFHTLIAYSDLYIINKLHVDESVEGSKTRR 130
DB 328 ----LFI-----TIAGVSG-----FHALISSGTPKMLENETHVRMIGYGMLE 370
QY 131 AFYLAAPFFMDAMAWTHAGI-LLKHYSFLVGCASISDVIAQV-----VFVAILLH 181
DB 371 SFVAIMA---LAAASLDPGVVFAMNSPAALIG--TDANTAREVITTKLOFPVDAATLLH 425
QY 182 SHLECREPLLIITLSLYMGALVRCCTLCGLGYKNHDIIPDRSGPELGDDATIRQWLSFW 241
DB 426 TAKEGEN---TILSRAGA---PTLAVGMHINSRLIP-----GEA-----MMAFW 466
QY 242 WPLALIL-----ATQIRSRPVLNLFVSRDLGG-----SSAATEAVAILTAT 282
DB 467 YHFAALLFEALFILTAVDAGTRVAR-----FMQDLGSIYKPFNGTDSIPANLIATFFAV 521
QY 283 YPVGMHPYGLWTE---IRAVYPAFDKKNPSKNKLVSTNTVTAHHKKFTFVCMALSLTL 338
DB 522 ALMGFLYTGVTDPGLGINSMLPLF-----GIANQMLA-----GVALLM 560
QY 339 CFVWF-----WTPNVSEKILIDIIGVDFAPAEFCVPLRIFSPFFPVVTVRAHUTG 389
DB 561 CAVVLIKMKRDRVWV-----VLVPAGVLFV---TCVAGLQKLFHSDPRISFLAHAGK 611
QY 390 WMLTKKTFVLAPS-----SVLRIL-----VLIASLVLPYLVGHGATLGVGSLIA 435
DB 612 YSDALAKNEILAPAKDIGEMAOIIFNDKINAGLTILFUSVWVI---VAAYGLRT---ALKA 666
QY 436 GFVGESTWVAIAACYVVRKQ 455
DB 667 RKVGWPTAKEIPAVYEDGKQ 686

RESULT 4
E81865
carbon starvation protein A homolog NMA1698 [similarity] - *Neisseria meningitidis* (stra
C:Species: *Neisseria meningitidis*
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: E81865
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: AB1775; MUID:2022556; PMID:10761919
A:Accession: E81865
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-693 <PAR>
A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CBM84926.1; PID:g73803.
A:Experimental source: serogroup A, strain Z2491

QY 408 -IIVLASLVLPYLVGHGATLGVSLAGFVGESTWVAIA 447
DB 403 FTLVICGSLIFTHSGATSAAYG---MLAGVSEIIVFLFA 440

RESULT 2
AH2537
hypothetical protein alr7587 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120be
C:Species: *Nostoc* sp. PCC 7120
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH2537
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2537
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-453 <KUR>
A:Cross-references: GB:AP003602; PIDN:BAB77230.1; PID:g17134672; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7587
A:Genome: plasmid

Query Match 7.1%; Score 180.5; DB 2; Length 453;
Best Local Similarity 20.4%; Pred. No. 4.2e-07;
Matches 94; Conservative 91; Mismatches 206; Indels 69; Gaps 15;
A:Residues: 1-453 <KUR>
A:Cross-references: GB:AP003602; PIDN:BAB77230.1; PID:g17134672; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7587
A:Genome: plasmid

QY 13 LIRFLVPLGINTIAIDFGEQALNRGTAAYKEDAVEMLASYGSLAYSLMKFTGPMSPDKV 72
DB 34 LLKQFIPLSLSDVAMTLDPLTSRLSPPO-ETLAVGVWGVAVFLESPIIMILHA 92
QY 73 GLVFNKRDRTKAVLCMVVAG-ALAAVFTLIAYSDLYIINKLHVDESVEGSKTRR 131
DB 93 STALGGQAKSRVLMQFTVIAGLALSGIF-LFLTWKPLYNMLLDDLPVSSIAARGTA 151
QY 132 FLYLAAPFFMDAMAWTHAGI-LLKHYSFLVGCASISDVIAQVFWVAILLHSHLE- 185
DB 152 FLLMFLPFWVIAWRRFFQGLLIRAKHSIAGVWASVARUTWIVTLAVGVSLRLDGAFLAG 211
QY 186 -----CREPLLIITLSLYMGALVRCCTLCGLGYKNHDIIPDRSGPELGDDATIRKWL 238
DB 212 IFMGAILIEAVLVWFLRLGALISILNO--QGVSET-----KKUPQTFGEVTF- 259
QY 239 SPWWPLALILATQIRSRPVLNLFVSRDLGSSAATEAVAILTATYPVGMHPYGLWTEI- 296
DB 259 -YVLPLASTMLLVWGARAILLSIARAFDGS-----IALAVMPAA---WGLLSLAN 306
QY 297 -----RAVYPAFDKKNPSKNKLVSTNTVTAHHKKFTFVCMALSLTLFCVWFVTPNVSE 350
DB 307 GTRMIQQVVISAYEE-----TSRRTLAFAV-----IIVGLSFTLIPFLGYTDQGL 352
QY 351 KILIDIGVDPAFAELCVVPLRIFGFFPVTVRAHLTGWMLTL-KKTFVLAPS SVLRIL 409
DB 353 FILRQFLGNPNLSVNASRVPQILSLCLPALLALONTFQGLLHKGNWFNLATIVRAIL 412
QY 410 VII--ASLVVLVYPYLVGHGATLGVSLAGFVGESTWVAIA 447
DB 413 TLVVCGLTIFTRHSGANSAYG---MLAGVIGEIIVLFFFA 449

RESULT 3
C81078
carbon starvation protein A homolog NMB1493 [similarity] - *Neisseria meningitidis* (stra
C:Species: *Neisseria meningitidis*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81078
R:Tetrelín, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

C:Genetics:
A:Gene: NMA1698
C:Superfamily: carbon starvation protein

Query Match 4.6%; Score 117.5; DB 2; Length 693;
Best Local Similarity 22.3%; Pred. No. 0.11;
Matches 100; Conservative 63; Mismatches 149; Indels 137; Gaps 24;

QY 62 FTGPMDFKNGVGLFVNSKRDRTKAVLCWVAGAAVFTLIIAYSDLGYYIINKLHVD 121
DB 320 FSGALFPE-----LPI-----TIACGVSG-----FHALISSGTTPKMLENETHVRM 361

QY 122 ESVGKTRRAFLYLAAPFMDAMAWTHAGI-LLKHYSFLVGCASISDVIAQV-----173
DB 362 IGYGMLMESFVAINA-----LAAASLDGVYFAMNSPAALIG--TDANTAEEVITTKLQF 416

QY 174 -VFVAILLHSHLECEPELLIPILSYMGALVRCCTTCLCGYYKNDIIPDRSGPELGDA 232
DB 417 PVDANTLHTAKEVEN--TILSPAGG--PFLAVGMHIMSRLIP-----GEA 461

QY 233 TIRKMLSPFWPALIL-----ATQISRPVNLVFSRDJGG-----SSAAT 273
DB 462 ---NMAFWYHFAALLFEALFILTAVDAGTRVAR-----FMQDLGSIYKPFNGNTDSTPA 512

QY 274 EAVAILTATYPVGHMPYGLTE---IRAVPAEDKNPNKLVSTNSTVTAAHKKFTF 329
DB 513 NLIAFFFAVALMGYFLYTGVTDPGLGINSLWPLF-----GIANQMLA-----554

QY 330 VCMALSLLTCFYMF-----WTPNVSEKILIDIIIGVFAFALCVVPIRIFSPFPV 380
DB 555 ---GVALLIMCAVLIKMKRDYVWV-----VLVPAVGLFV---TCVAGLQKLFHSDPR 602

QY 381 VTVRAHLTGWMLTKKTFVLAPS-----SVLRIT-----VLIASLVNLPVLGVHGA 426
DB 603 ISFLAHTGYSDALAKNEVLAPAKDIGEMAQIIFNDKINAGLTILFLSVVVI--VAAYGL 660

QY 427 TLGVGSLLAGFVGSESTVMAIACYVRKQ 455
DB 661 RT---ALKARKVGMFTAKEIPAVYRDGKQ 686

RESULT 5

S78182
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Reclinomonas americana (ATCC 50394)
C:Species: mitochondrion Reclinomonas americana

A:Variety: ATCC 50394
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
C:Accession: S78182

Ribang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank
Nature 387, 493-497, 1997
A:Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature.

A:Reference number: S78127; MUID:97311393; PMID:9168110
A:Accession: S78182
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-670 <LAN>
A:Cross-references: EMBL:AF007261; NID:G2258325; PIDN:AA11915.1; PID:G2258381

A:Experimental source: ATCC 50394
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997
C:Genetics:

A:Gene: nad5
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.6%; Score 115.5; DB 2; Length 670;
Best Local Similarity 19.1%; Pred. No. 0.16;
Matches 94; Conservative 72; Mismatches 191; Indels 135; Gaps 19;

QY 5 PALTHYWPILRIFVPIGNTN-----IADFGEQALNRGIAAVKEDAV 46
DB 111 PRFMSYLSLFTFFMLMLVITGDNFVQMFGLGWEGVGLCSYLLINFWFRLLQANKSAIKAMIM 170

QY 47 EMLASYGLAYSLMK-FTGPMDFKNV-----GLVFNYSKRDRTKAVLCWVAGA 95
DB 171 NRIGDFGLSLGMAIFTFKSDVFTVFALSPYMTDFNIIFFNVEVHALTICILLFVGA 230

QY 96 IAAV-----PHTLIAYSDLGYYIINKLHVDSEVGSKTRRAFLYLAAPFMD-----142
DB 231 VGKSSQLGHTLWPDAMEGPTTPVSALIIHAATWV---TAGVFLIARCSPIFEVAPTALLVV 287

QY 143 ----AMAWTHAGI-LLKHYSFLVGCASISDVIAQVVFVAILLHS-----HLECREPLLI 192
DB 288 TIVGAMTAFAATTGLQNDIKRVIAYSTCSQLGYVVFACGISGYSGVMFHL-----339

QY 193 PILSLYMGALVRCCTTCLGYKYNHDIIPDRSGPELGDDATIRKMLSFWMPLALIIATQR 252
DB 340 -MNHAFKALLFLSAGCV-----IHALADEQDMRMGG---IVKIVFFYGMMLIGMSML 390

QY 253 ISRPVNLVFSRDLGSSAATAEAVAILTATYPVGHMPYGLWTEIRAVYPAF-----303
DB 391 MGPFELTGFSKDV-----ILELAFAKYITDGTFAHWLGTVAAPFTAFYSFRLLYLT 442

QY 304 ---DKNPNKLVSTNTVTAHIKF--TFVCMALSLLTCFYMFVTPNVSEKILIDIIIG 358
DB 443 FLGETNSP-----RTIINHARDAFFIMAFPLMILAVGSI FVGF---VMKDMMIG-LG 490

QY 359 VDFAFALCVVPIRIFSPFPVTVRAHLTGWMLTKKTFVLAPSSVLRIIIVLIASLVVL 418
DB 491 TDFWNSLTHPKN-----LTLIESEFIPTPKLLPV-----523

QY 419 PYLGVHGAATLV 430
DB 524 --LSITGATLAI 533

RESULT 6

PTS betaglucoside-specific enzyme IIC component homolog lmo0373 [imported] - Listeria mo
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AF1121

R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1121
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-444 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC98452.1; PID:G16409751; GSPDB:GN00177
A:Experimental source: strain EGD-e

C:Genetics:
A:Gene: lmo0373
C:Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depend

Query Match 4.6%; Score 115; DB 2; Length 444;
Best Local Similarity 20.4%; Pred. No. 0.11;
Matches 94; Conservative 69; Mismatches 151; Indels 146; Gaps 25;

QY 66 MSDFKNV-----GLVFNYSKRDRTKAVL-CWVAGAAIAAVFHTLIAYSDLGYYIINKLH 119
DB 10 VNGFINAQLGGQIHLSRIRDAFASIMPPMILAG-----FVTLI-----NYVILEPTGF 59

QY 120 VDESVGSKTRRAFLYLAAPFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVVFVAIL 179
DB 60 MGKIVNPTDLR-----TWQEIGI-----SIGNGTLS-VITLLVTVAIS 96

QY 180 LH-----SHLECREPLLIPLISLYMGALVRCCTTCLGYKYNH--DIIP-----DRSGPEL 228
DB 97 YHLCINRGYNVIAPILVALSSFIWVTPITAMTFLPEGASKSIEVPNVIPVSTGASGMFV 156

```
QY 229 G-----GDATIR-----KMLSFWMPLALILATQIRSRPIVNL 261
Db 157 GIIVGLTATDLFKLSKSKRMQINLTGNIPAVKSNVLIPIIMITVIFSVMSFAVNI 216
QY 262 VSRDLGG--SSAATEAVAILTATVPVGHMPYGM--TEIRAVY-----PAFDK 305
Db 217 FSDMNTLVITITIKPLSVYVTSLSF-----GFLITSIANLPFGLGHOAVISGILLDP 270
QY 306 ---NNPSNKLVSNTVTAHI---KKFTFCVM-----ALSITLCFVMEW----- 344
Db 271 FLLQMOENWVAYANHOEIPHIINNAFKOTFANVGGSGNTIGLLIAIFIGKKKQYKDIS 330
QY 345 ----TP---NVSEKILIDIIGVDFAFELCVFLRIFSFPPVTVRAHLTGWL--MTLK 395
Db 331 KLSAAPSLENISEPI---IFGLPIVFNPLLIIPVLAPIESLTTAYVATAAGNINHWVQ 387
QY 396 KTFVLAP-----SSVLRILVLIASL-VLPLYL 421
Db 388 TPWTTPPIISGFLATGDNRASVLQVLIIVTVPIYLPFL 427

RESULT 7
B83988
Proline transporter opuE [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B83988
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83988
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <STO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06425.1; GSPDB:GNOC
A:Experimental source: strain C-125
C:Genetics:
A:Gene: opuE
C:Superfamily: proline carrier protein

Query Match 4.6%; Score 115; DB 2; Length 507;
Best Local Similarity 21.1%; Pred. No. 0.13;
Matches 115; Conservative 75; Mismatches 186; Indels 168; Gaps 25;
QY 45 AVEMLASVGLAYSMKFTGP-----MSDF-----KN-----VGLFVNSKRDRTKAVLCM 90
Db 8 AVAILIYVALLITGLLSKSSVGMTPDFIAGRNKNKWTVALSAVSSGR---SAMLVL 64
QY 91 VWAG-----AJAAVFHTLIAYSDLYIINKLHHVDESVS-----KTR----- 129
Db 65 GWTGTAVATGLDVAWVAGYITVEVFLFFVARRFRAYSQTGSIITPIDILETRFNDKTH 124
QY 130 -----RAFL---YLAAF-----PMDAMA-----WTHAGILLKHKYSFLVYGA 164
Db 125 ILRGSATFIIMFFMIAYVASQLVAGGAFATSMGVSSSTGMWTVAVILL---AVTMLGGFH 182
QY 165 SIS--DVI--AQVVFVAILLHSHLECPFLIPILSLY-----VILPVVAIIIGLGGDFLLQVMHTEGGFTSPF 198
Db 183 AVSKTDVVQAGFMFVSL-----VILPVVAIIIGLGGDFLLQVMHTEGGFTSPF 231
QY 199 ---MGALVRCCTLCIGYKYNHDIIPDRSGPELGGDATIRKMLSFW-----WPLALILAT 250
Db 232 AFGGAVTGLLIGIGSGSPGNPHILVRYNSLKNVKNEMQAALISSVMNVLWGAVMIGLA 291
QY 251 ORISRPVNLVFSRDLGGSSAATEAVAILTATVPVGHMPYGM--TEIRAVYPAFDKKNPSN 310
Db 292 GRAYFPDVLSPNGD-----QEQVFLMGLSEILHPLFFGFL--LVAVLAAMSSADSQ 342
QY 311 KLVSNTNTVTAHIKKF-----TFVCMALSLTLCFV-----MFTWPNV 348
Db 343 LLVGSSAFVRIYQRMFRNRKLSQKLVRLSLRTTVVFMGLSLILAFTAQEFVFWV--- 399
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QY 349 SEKILIDIIGVDFAFEL--CVVPLRIFSFPPVTVRAHLTGWLMTLTKKTFVL--APSS 404
Db 400 -----VLFAPGGLGACFGPALLLSFYKWKVTRQGVLMGMIAGLLVILVKQGPQW 449
QY 405 VLRIIVLIASLVLPYLVGHGATLGVGSLLAGFVGESTMVAIAACYVYR-----KQKKQME 460
Db 450 TYARLPDVKELLNTVFFGI-----TVEAVPGFIVATTITVVISLTKRPRKHAQIIERL 503
QY 461 NESA 464
Db 504 NESA 507

RESULT 8
F69433
conserved hypothetical protein AF1471 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
C:Accession: F69433
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischiemann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: F69433
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-447 <KLE>
A:Cross-references: GB:AB001001; GB:AB000782; NID:G2689324; PIDN:AAB89777.1; PID:G26490;
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0709

Query Match 4.5%; Score 114.5; DB 2; Length 447;
Best Local Similarity 21.1%; Pred. No. 0.12;
Matches 97; Conservative 78; Mismatches 164; Indels 121; Gaps 24;
QY 19 PLGITNIAIDEG-----EQALNRTGIAVKEDAVEMLASVGLAYSMKFTGPMDFKNVG 73
Db 56 PIFFVFIASISGLSVGANSVSRIRGAKRYDAACVAATLAVANGLL--VSIPMT-----LS 109
QY 74 LVFVNSKRDRTKAVLCMVVAGIAAIVFHTLIAYSDLYIINKLHHVDES-----GSK 127
Db 110 VVFLNG-----VWVFLGADGELRLAVDYGSI--MWLGSVFLVFSNVSAGILNGEG 158
QY 128 TRAPLYLAAPFPMDAMAWTAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLECR 187
Db 159 NARMAMYANA-----AGSLNMMVLDPIFYLLGYGIAGAAIASVISMAL----- 202
QY 188 EPLLIPILSLYMGALVRCCTLCIGYKYNHDIIPDRSGPELGGDATIRKMLSFW----- 241
Db 203 -----SSIVFSFW-----FLSGRSYVAFRVAGNMLPTVF 231
QY 242 -----WPLALILATQIRSRPIVNLVFSRDLGGSSAATEAVAILTATVPV---GHMP-YG 291
Db 232 DLRLVGMFASLSMLTMSVAFMLINRWVI--ETGGS-----EGLAAYTSAWRLIQFGFVPLFG 286
QY 292 WLTEIRAVY--PAFDKKNPSNKLVSNTVTAHIKKFTFVCMALSLTLCFVFMFTWPNV 350
Db 287 VSAALTAVSAGYAGARNPRKIGESLNTV-----KLLAVDAAI--LALVAFAPQIA- 337
QY 351 KILIDIIGVDFAFELCVVPLRIFSF-----PVPVTVRAHLTGWLMTLTKKTFVLAPSSVL 406
Db 338 -LIFTYTEVSATVMEIEIVRTIRAFVLLFAPLGVSSSAVFQG-MGKGRSFAT---TVL 392
QY 407 RIIVLIASL---VLPYLVGHGATLG--VGSILAGFVGES 441
Db 393 RAIVQVSLCYLVAVFP--GFDGVLGFLVGLGALGCTGFS 431

RESULT 9
E89978
```

high affinity proline permease [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: E89978
R;Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: E89978
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-512 <CUR>
A;Cross-references: GB:BA000018; PID:g13701695; PIDN:BAB42988.1; GSPDB:GN00149
A;Experimental source: strain N315
C:Genetics:
A:Gene: putP
C:Superfamily: proline carrier protein

Query Match 4.58; Score 113.5; DB 2; Length 512;
Best Local Similarity 18.88; Pred.No. 0.17; Indels 173; Gaps 17;
Matches 90; Conservative 66; Mismatches 149;

QY 53 GLAYSLMKFTGPMSPDKNYGLVFNVSKRDRTRAVLCWVVAGAIATAVFHTLIAYSILGY 112
Db 117 GDATITLPDFEKNRLNDKNV-----LKIISGLIIVVFETL--YTHSGPV 158
QY 113 IINKLHVDESVCSTRARLYLAAPFMDAMAWTHAGILLKHYSFLVG--CASISDVI 170
Db 159 SGCKLF---ESAFGLDYHFGILIIVAF-----IVIFYTFPGGYLAVSITDF 201
QY 171 AQVFFVAILLRHSHLECREPLIPI-----LSLXWG----ALVR 204
Db 202 QGVIMLIAM-----VWPVIVMMNLNGWTFHDVAAKPPTNLNFKGLSFGIIS 251
QY 205 CTTLCLGYKNIHDIIPDRGPBLGGDATIRKMLSFWWPLAL----- 246
Db 252 LFSWGLGYFGQPHTIIVRFMSIKSKHMLPKARRLGISMVAVGLIGAVAGLTGAIFVPAYH 311
QY 247 -----ILATORISRPIVMVLFRSDRLGGSSAATEAVAILTATYPVGHMPVGMLETI 296
Db 312 IKLEDPTFLIVMSQVLFHPLV-----GGFLIAAILAAIMSTI----- 349
QY 297 RAVYPADFKNPNKGLYSTNTVT-----AAHIKKFTFCMALSLTLCFV-- 341
Db 350 -----SSQLLVTSSTLTDYFKLRGEAKTKHQERVMIGRLSVLVAIVA 397
QY 342 -MFWTPNVSEKILIDIICVDPAFAELCVBLRPFSPFPVTVRAHLTGMLTKKTFTVL 400
Db 398 AIANWNP-----DTILNLVGNWAGFGASFSPLVLFALYWKGLTRAGVSGMV----- 445
QY 401 APSSVLRIIIVLIASLVPLPVGHGATLGVSLGFVGESTMWVIAACVYVRKQKK 458
Db 446 --SGALVVIWIAWIKELAHI---NEIFGLYEIIIPGI-----VSVIVTVVSKLTTC 493

RESULT 10
S02154
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Podospora anserina mitochondrion
N;Alternate names: NADH-ubiquinone oxidoreductase chain 2
C:Species: mitochondrion Podospora anserina
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 03-Jun-2002
C:Accession: S02154
R;Cumings, D.J.; Domenico, J.M.
J. Mol. Biol. 204, 815-839, 1988
A>Title: Sequence analysis of mitochondrial DNA from Podospora anserina
A;Reference number: S02153; MUID:89125610; PMID:2975708
A;Accession: S02154
A:Molecule type: DNA
A;Residues: 1-556 <CUR>
A;Cross-references: EMBL:X14485; NID:g13296; PIDN:CAA32646.1; PID:g13297
C:Genetics:

A;Gene: ND2
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.5%; Score 113.5; DB 2; Length 556;
Best Local Similarity 19.5%; Pred. No. 0.19; Indels 169; Gaps 21;
Matches 94; Conservative

QY 13 LIRPL-----VPLGITINIAIDFGQALN-----RGIAAVKEDAVEMLA-----SYG 53
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 177 LIYFLGLSSCFILLGTSLIYINSNGTISLDGLVILNSISDVKDGAAMPALTSWYKSVY 236
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 54 IAYSIMKPFPTGMSDFKNVGLVFVNKRDRTKAVLCVMVAGAAVFTLIAYSDLGYYI 113
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 237 LNFAALVESIGFL--FKVSAAPEHFWSPPVDAL-----PTIVTFVAIIAKISIFIP 288
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 114 INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVCASISDVIQV 173
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 289 LELVVHTNN-----YLSEF-----SWTYL-LLSLSFLSIIGTVV---GLTQF 327
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 174 VFVAILLHSLECREPLLIPILSYMALVRCCTTLCLGYVKNIHDIIPDRSGPELGGDAT 233
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 328 RIKELLAYSTIS-----HVGFILLALSGC-----S 352
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 234 IRKMLSFWMPPLALILATQRISRPNLVNFVSRDLGSSAATEAVAILTATYPVGHMPCWL 293
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 353 IESTQAIFIYV-----IQYSISNLNV-----FIILT---IGFSLYGI 388
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 294 TEIRAVYPAPDKNNPSKNLSTNTVTAAHIKFFVCMALSLTLCFMFWPVPNVSEKIL 353
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 389 TTNKEYKDLLDKNNSPQVTS-----QLKGIFYINPLLSLAITIF----- 430
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 354 IDIIG----VDFAFAEICVPLRFSPFPVTVRAHLTG-----WMTLKKTFLVLP- 402
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 431 -SFVGIPPLVGP-FAKQNWLSAADNGY-IFLTIALITSVIGAVYYINIIRKIFFYLPD 487
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 403 -----SSVLRIIVLIASLVVLPYLVGHGATLVGS 432
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 488 HSINPSIGEFLFKKGLIFEAGDFKGRITLISSPFSIISIITLVLLPIFNKEWLSMG 547
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 433 LL 434
| | : | :
DB 548 IL 549

RESULT 11
AD0828
probable transmembrane transport protein STY2820 [imported] - Salmonella enterica subsp.
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AD0828
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronan, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Meule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero-
A;Reference number: AB0502; UID:21534947; PMID:11677608
A;Accession: RD0828
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <PAR>
A;Cross-references: GB:AL513382; FIDN:CAD02776.1; PID:g16503786; GSPDB:GN00176
C;Genetics:
A;Gene: STY2820
C;Superfamily: hypothetical protein c0103

Query Match 4.5%; Score 112.5; DB 2; Length 398;
Best Local Similarity 19.3%; Pred. No. 0.15;
Matches 93; Conservative 69; Mismatches 136; Indels 183; Gaps 24;

QY 3 KFPALHY-W-----PLIRFLVPLGITNIAIDFQEQALNRGIAAIVKEDAVEMLASGLAYS 57
Db 31 KTLMAQYHWDPAALAFSINMGIIPLPMWIGGRMIDNG-----KGQAIIVIGGILFS 84
QY 58 L-----MKFTGPMSPDKNVGLVFVNSKR-----DRTKAVLCWVAGIAIA 98
Db 85 LGFILSGFVNLPMLFUTYGVIAGLSGLAFTGNLNNILKFFPDRLGLASGIVLAGVG 144
QY 99 VFHTLIAYSDIGYIINKLHHVDSVSGSKTRRAFLYLAAPFFMDAMAWTHAGILLKHYS 158
Db 145 ---TLLC-TRLAEFMAQTHDVS-----RALLYLG----- 170
QY 159 FLVCCASISDVIAQVFAVAILLHSHLSREPLLIPIILSLYMGALVRCITTLCLGYKNKIH 218
Db 171 -----IVLVVIF-----IVQFFI----- 184
QY 219 IIPDRSGP-BLGG-----DATIRKMLS-FWFLALILATORISPIVNLVSRDLG- 267
Db 185 ---RSAPAKDSGGIKASPLDKDYRHKMLDLRFLLFMILALGVFSGMWIS-SSSAQIGM 239
QY 268 ---GSSAATEAVAILTATYPVGHMYPYGNLFEIRAVYAFDKNPSNKLVSSTNTVTAHI 324
Db 240 TQYGLLSGALVSVLSFNSIGRLFWGLTDLGGY-----NTLVIVYL 283
QY 325 KKFTFVCVALSITLCFVNFMTNPNVSEKILIDIGVDFAFELCVVPLRI----- 373
Db 284 ---FICVCMLL-----LLFFNGTNS-VYFSAVGGRAYAGILVIFGLTSQNFGRNQ 334
QY 374 ---PSFP-----PVPTVTRAHLTGMLTKTFLVAPSSVLRILVILASLVLPY 420
Db 335 LNYGPMYEGFAVAGIAPVYVTSIAKYTGSYNTV---FIL---TTVLLIGVVLTLTKY 389
QY 421 L 421
Db 390 V 390
RESULT 12
T48676
proline uptake protein [validated] - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C:Accession: T48676
R:Schwan, W.R.; Coulter, S.N.; Ng, E.Y.; Langhorne, M.H.; Ritchie, L.L.; We
Infect. Immun. 66, 567-572, 1998
A:Title: Identification and characterization of the PutP proline permease that contribut
A:Reference number: Z24528; MUID:98114355; PMID:9453610
A:Accession: T48676
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-497 <SCCH>
A:Cross-references: EMBL:AF024571; NID:G2565310; PIDN:AAC38087.1; PID:G2565311
A:Experimental source: strain RN6390
C:Genetics:
A:Gene: putP
C:Function:
A:Description: involved in proline uptake [validated, MUID:98114355]
C:Keywords: amino acid transport; proline transport; transmembrane protein
Query Match 4.5%; Score 112.5; DB 2; Length 497;
Best Local Similarity 18.8%; Pred. No. 0.2;
Matches 90; Conservative 66; Mismatches 149; Indels 173; Gaps 17;
QY 53 GLAYSLMKFTGPMSPDKNVGLVFNNSKDRYKAVLCWVAGIAAIVPHTLIAYSGLGY 112
Db 116 GDAITLPDFFKRLNDKNNV-----LKIISGLIIVVFTTL--YTHSGFV 157
QY 113 IINKLHHVDSVSGSKTRRAFLYLAAPFFMDAMAWTHAGILLKHYSFLVG--CASISDVI 170
Db 158 SGKLPF---ESAFGLDYHGLILVAF-----IVIFYTFGGYLAVSITDFF 200

QY 171 AQVVFVAILLHSHLECREPLLIPI-----LSLYMG-----ALVR 204
Db 201 QGVIMLIAM-----VMPPIVAMNUNGWGTTFHDVAMKFTNLFKGLSFIGIIS 250
QY 205 CTTCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWMPLAL----- 246
Db 251 LFSWGLGVFGQPHIIVRFMSIKSHKMLPKARLGLISWMAVGLLGAVAVGLTGIAFVPA 310
QY 247 -----ILATQISRPVNLVSRDLGSSAAATEAVAILTATYPVGHMYPYGLTEI 296
Db 311 IKLEDPETLFVMSQVLFHPLV-----GGFLAILAALAIMSTI----- 348
QY 297 RAVYPAFDKNNPSNKLVSSTNTVT-----AAHIKFTFVCMALSLTLCFV- 341
Db 349 -----SSQLVTSSTLTDFYKLIRGEEKAKTHQKFFVMIGRLSVLVVAIVAI 396
QY 342 MFWTPNVSEKILIDIGVDFAFELCVVPLRIISFPFVPTVTRAHLTGMLTKLTKTEVL 400
Db 397 ATAMNPN---DTILNLVGNWAGFGASPLVLFALYWKGLTRAGAVSGMW- 444
QY 401 APSVLRITVILIASLWPLVGLVGHGATLGVGLAGFVGESTMVAIAACYYVRKQKK 458
Db 445 --SGALVIVWIAWKPLAHI---NEIFGLYEIIIPFI-----VSVIVTVVVSUKTKK 492
RESULT 13
E69609
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bacillus subtilis
N:Alternate names: caa3-605 cytochrome-c oxidase chain I; cytochrome-aa3 chain I
C:Species: Bacillus subtilis
C>Date: 08-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E69609; S14397
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte;
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
A.; Lech, J.; Harwood, C.R.; Renaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Fortetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyana
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yosikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69609
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-622 <KUN>
A:Cross-references: GB:Z99111; GB:AL009126; NID:G2633699; PIDN:CAB13363.1; PID:G2633661
A:Experimental source: strain 168
R:Saraate, M.; Metso, T.; Nakari, T.; Jalli, T.; Laureus, M.; van der Oost, J.
Eur. J. Biochem. 195, 517-525, 1991
A:Title: The Bacillus subtilis cytochrome-c oxidase. Variations on a conserved protein
A:Reference number: S14395; MUID:91146590; PMID:1847686
A:Accession: S14397
A:Molecule type: DNA
A:Residues: 1-119, 'G', 121-154, 'SI', 157-287, 289-473, 'R', 475-622 <SAR>
A:Cross-references: EMBL:X54140; NID:9994793; PIDN:CAA38077.1; PID:G939870
A:Experimental source: strain W168
C:Genetics:
A:Gene: ctad
C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-a
F:23-467/Domain: cytochrome-c oxidase chain I homology <CO1>
F:27-43/Domain: transmembrane #status predicted <TM1>
F:78-94/Domain: transmembrane #status predicted <TM2>
F:107-123/Domain: transmembrane #status predicted <TM3>
F:161-177/Domain: transmembrane #status predicted <TM4>
F:203-219/Domain: transmembrane #status predicted <TM5>

Matches	95;	Conservative	68;	Mismatches	140;	Indels	133;	Gaps	22;		
QY	55	AYSIMKFTGPMDFKNVGLVTV--NSKRDRTKAVLCMVVAGAAIAVFTLLI-----AYS	107								
DB	61	AYILFAPFVGQIADSFAGKRVMMVANGKLGAAGICL--GVNPFVGYTLVGIGAAAYS	117								
QY	108	DLGYIINKLHHVDVSGSKTRRAFLYLAAPFFMDAMANTHAGILLK--HKYSLVGC-	164								
DB	118	PAKYGILGEL-----TTGDKLVKANGLMEASTTAAILLGSVAGGLADWHVIAALVACAL	172								
QY	165	SISDVIAQVVFVAILLHSHLECREPLILPILSYMGALVR---CTTLCGLGYXN---IHD	218								
DB	173	AYAGAVAAFLFIPKLVAAAR-----PGQSWRLSAMTRSFFFCA--CVVLMRNGETRFS	221								
QY	219	IIPDRSGELGSDATIRKMILSFMWPLALILIAIATORISRPVNLFSRDL-GGSSAATAVA	277								
DB	222	LV--GTGLFWGAGVTLREFLLVWLPVALGI--TDNATPTYNAMVAVGIVGAGAAKLVT	278								
QY	278	ILTATYPVGHMPYGMWLTEI-----RAYVPAFDKNNPSNKLVTSTNTVTAHHKKFTF	329								
DB	279	LETVS--RCMPAGILIGVVVAIFSLQHALLPAY-----	309								
QY	330	VCMAISLTLFCWFMTWPNVSEKILIDIIIGVDFAELCVVPLRFSRFPVPTVRAHLTG	389								
DB	330	---ALL-----LIGMLG-----GFFVPEINALLQBERG	334								
QY	330	WLMTLKTF-----VLAPSSVLRIRIIVLIASLWLVLYLGVHGATLGVGSLLAGFVGE	440								
DB	335	---KKSVGAGNATAVQNLGENSEAMLLMLGLSLAVL--VGVPVAIGIG-----FGV	381								
QY	441	STWVAIAACYVRKOK	456								
DB	382	LFALAIALAIWQRQ	397								
RESULT	15										
AB1437											
		PTS system, cellobiose-specific IIC component homolog lin0033 [imported] - Listeria inno									
		C:Species: Listeria innocua									
		C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001									
		C:Accession: AB1437									
		R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker									
		D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.									
		D.; Jones, L.M.; Karst, U.									
		Science 294, 849-852, 2001									
		A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma									
		ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,									
		A:Title: Comparative genomics of Listeria species.									
		A:Reference number: AB1077; MUID:21537279; PMID:11679669									
		A:Accession: AB1437									
		A>Status: preliminary									
		A:Molecule type: DNA									
		A:Residues: 1-452 <GLA>									
		A:Cross-references: GB:AL592022; PIDN:CAC95266.1; PID:gl6142454; GSPDB:GN00178									
		A:Experimental source: strain Ciip11262									
		C:Genetics:									
		A:Gene: lin0033									
		C:Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depend									
		Query Match	4.4%;	Score	110.5;	DB	2;	Length	452;		
		Best Local Similarity	18.5%;	Pred. No.	0.26;						
		Matches	92;	Conservative	86;	Mismatches	173;	Indels	145;	Gaps	23;
QY	59	MKEFTGPMDFKNVGLVFNVSKRDRTKAVLCMVVAGAAIAVFTLLIAYSGLGYIINKLH	118								
DB	15	LSIFAQIKSQHHWAI-----RDFRAMIPTIIRAFLLVNNVLLQPENG--LLKPTP	67								
QY	119	HYDESYG-----SKTRRAFLYLAAPFFMDAMANTH-----GILLKHKYSFLVGCAS-	165								
DB	68	NVENYLGVGQVYNATLGMILAAFLIGNFLAKSGYMEGRTEGMVAAYAVVLPASSH	127								
QY	166	ISDVIAQVVFVAILLHSHLECREPLILPILSYMGALVRCITLCL-GYXNHIHDIIPDRS	224								

Db 128 LMSYDGKAFAGGYLTQEMTSSTGMFLAIIA-----SLVSITMLAKFSKSLKISMPESV 183
Qy 225 GPELGGDATIRKMLSFWMLALILATQISRPVNLVSRDL-----GGSSA 271
Db 184 PP-----ATAKSFNIIIPSFVLISLAIIEVLVSVFVMSIPEIIVKVQIPLVGGFOT 237
Qy 272 ATEAVAILTATYPVGHMPCYGNLFEIRAVYPAFDKNNPSNKLNVST----- 316
Db 238 LP---GILLYVFLAGFL---W---VFGIHGAFVLGAISGFVLITSLQONIDAVNAGTALP 288
Qy 317 NTVTAHIKKF-----TFVCMALSLTLCFVMEWTP-----NVSEKILI 354
Db 289 NIVTQPELDAFVVMGGGTIIICLVIAI---FIASKRPDHRMVTKFGIIPSFNVSEPLM- 344
Qy 355 DIIGVDPAFAELCVPLRIEFPFVPTVRAHIT---GNLMTLKKTFVLAP----- 402
Db 345 --FGLPVVFNPIYGIPLVI---APLASTAMAYFATSWGW---ISQVILIPWVTPPVLSG 396
Qy 403 -----SSVLRI-IVLIASLVWLPYLGVHGATLGVGSLLAGFVGESTMWAIACVY 452
Db 397 YLATGGDIRASIIQIAIIVVGTLLIYDPFV-----LVANRAYVLE 435
Qy 453 RKQKKXKXENESATEGE 468
Db 436 QKAAGNVEAETVTNGE 451

Search completed: April 22, 2004, 13:58:28
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:50:23 ; Search time 18 Seconds
(without alignment)
1423.251 Million cell updates/sec

Title: US-09-978-188A-7
Perfect score: 2527
Sequence: 1 MVKFPALTHWPLRFLVPL.....TDMPTTEVTDIVEMRENE 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2527	100.0	492	1 ANKH HUMAN	Q9hjc1 homo sapien
2	2502	99.0	492	1 ANKH MOUSE	Q9jh22 mus musculus
3	2489	98.5	492	1 ANKH RAT	P58366 rattus norv
4	2317	91.7	492	1 ANKH XENLA	P58367 xenopus lae
5	2158.5	85.4	501	1 ANKH BRARE	P58368 brachydanio
6	1528.5	60.5	355	1 ANKH TETNG	P58369 tetraodon n
7	114	4.5	416	1 LACY KLEOX	P18817 klebsiella
8	113.5	4.5	556	1 PT2A PODAN	P15578 podospira a
9	111	4.4	622	1 COX1 BACSU	P24010 bacillus su
10	109.5	4.3	610	1 PT2A ARATH	P46031 arabidopsis
11	107	4.2	432	1 EXUT BACSU	O34456 bacillus su
12	107	4.2	533	1 LAT2 RAT	Q3wvr6 rattus norv
13	106	4.2	334	1 YB77 METJA	Q58578 methanococc
14	105	4.2	401	1 LSG1 HAEIN	P71399 haemophilus
15	105	4.2	676	1 HPPI METAC	Q8tja9 methanosaar
16	103.5	4.1	398	1 BCR HAEIN	P45123 haemophilus
17	103	4.1	417	1 LACY ECOLI	P02920 escherichia
18	102.5	4.1	446	1 CITN SALTY	P31604 salmonella
19	102.5	4.1	531	1 LAT2 MOUSE	Q9gxw9 mus musculus
20	102.5	4.1	533	1 NVIN RHIRT	O05467 rhizobium t
21	102.5	4.1	641	1 MNSM ALIMA	P03365 allomyces m
22	101.5	4.0	446	1 CITN SALDU	P31603 salmonella
23	100	4.0	982	1 YS96 CAELU	Q09965 caenorhabdi
24	99	3.9	395	1 Y421 METTH	O26521 methanobact
25	99	3.9	535	1 LAT2 HUMAN	Q9ubi5 homo sapien
26	98.5	3.9	593	1 NU2M NUOCR	Q35140 neurospora
27	98.5	3.9	946	1 YB76 YEAST	P38250 saccharomyc
28	98	3.9	480	1 YEH4 YEAST	P39981 saccharomyc
29	98	3.9	532	1 YABM BACSU	P37555 bacillus su
30	97.5	3.9	346	1 FMLR PONPY	P79235 pongo pygma
31	97.5	3.9	3803	1 TRAI DROME	O818u7 drosophila
32	97	3.8	402	1 YYCB BACSU	P37482 bacillus su
33	96.5	3.8	346	1 FMLR_GORGO	P79176 gorilla gor

34	95.5	3.8	416	1 LACY CITFR	P47234 citrobacter
35	95.5	3.8	483	1 NORM_VIBVU	O8d9n8 vibrio vuln
36	95	3.8	457	1 NORM_ECOS7	P58154 escherichia
37	95	3.8	459	1 NU4M BALPH	P24975 balaeopter
38	95	3.8	460	1 NU4M ASTPE	P11992 asterina pe
39	95	3.8	464	1 NORM HAEIN	P45272 haemophilus
40	95	3.8	501	1 LYSI CORGL	P35855 corynebacte
41	95	3.8	511	1 ALG8 DROME	O9w3v8 drosophila
42	95	3.8	654	1 NUSM RHIST	P50367 rhizopus st
43	94.5	3.7	507	1 TT12 ARATH	Q9lyc3 arabidopsis
44	94.5	3.7	518	1 SP5B BACSU	Q00758 bacillus su
45	94	3.7	421	1 VG2_BPIKE	P03660 bacterioph

ALIGNMENTS

RESULT 1
ANKH_HUMAN
ID ANKH_HUMAN STANDARD; PRT; 492 AA.
AC Q9HCJ1; Q9NQW2;
DT 28-PEB-2003 (Rel. 41, Created)
DT 28-PEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Progressive ankylosis protein homolog (ANK).
GN ANKH OR KIAA1581.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20355194; PubMed=10894769;
RA Ho A.M., Johnson M.D., Kingsley D.M.;
RT "Role of the mouse ank gene in control of tissue calcification and
RT arthritis";
RL Science 289:265-270(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hiroawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozney K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP VARIANTS CMDJ SER-375 DEL; PHE-376 DEL AND ALA-380 INS.
RX MEDLINE=21313103; PubMed=11326338;

Reichenberger E., Tiziani V., Watanabe S., Park L., Ueki Y.,
 Santana C., Baur S.T., Shiang R., Grange D.K., Beighton P.,
 Gardner J., Hamersma H., Sellars S., Ramesar R., Lidral A.C.,
 Sommer A., Raposo do Amaral C.M., Gorlin R.J., Mulliken J.B.,
 Olsen B.R.;
 "Autosomal dominant craniofacial dysplasia is caused by mutations
 in the transmembrane protein ANK";
 Am. J. Hum. Genet. 68:1321-1326(2001).
 [5]
 VARIANTS CMDJ ARG-292; ARG-331; SER-375 DEL; ALA-380 INS
 AND ARG-389.
 MEDLINE=2125282; PubMed=11326272;
 Nuernberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,
 Ritter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,
 Goldblatt J., Borochowitz Z.U., Kotz D., Westermann F., Mundlos S.,
 Braun H.-S., Laing N., Tinschert S.;
 "Heterozygous mutations in ANKH, the human ortholog of the mouse
 progressive ankylosis gene, result in craniofacial dysplasia";
 Nat. Genet. 28:37-41(2001).
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic
 pyrophosphate (PPi), probably functioning as Ppi transporter.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Found in osteoblasts from mandibular bone and
 from iliac bone; not detected in osteoclastic cells.
 CC -!- DISEASE: Defects in ANKH are the cause of craniofacial dysplasia
 (dysplasia Jackson type (CMDJ) [MIM:123000]). CMDJ is a rare
 autosomal dominant skeletal disorder characterized by abnormal
 bone formation and mineralization in membranous as well as
 endochondral bones. Progressive thickening of the bones can cause
 narrowing of cranial foramina and can lead to severe visual and
 neurological impairment, such as facial palsy and deafness.
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 the European Bioinformatics Institute. There are no restrictions on its
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF274753; AAF88039.1;
 DR EMBL; BAB13407.1; ALT_INIT.
 DR EMBL; BC009835; AAH09835.1;
 DR EMBL; BC014526; AAH14526.1;
 DR Genbank; HGNC:15492; ANKH.
 DR MIM; 605145;
 DR MIM; 123000;
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0019867; C:outer membrane; TAS.
 DR GO; GO:0030504; F:inorganic diphosphate transporter activity; IDA.
 DR GO; GO:0005315; F:inorganic phosphate transporter activity; IDA.
 DR GO; GO:0007626; P:locomotory behavior; NAS.
 DR GO; GO:0030500; P:regulation of bone mineralization; TAS.
 DR GO; GO:0001501; P:skeletal development; NAS.
 KW Transport; Phosphate transport; Transmembrane; Disease mutation;
 Deafness.
 KW
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 POTENTIAL.
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 132 152 POTENTIAL.
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 179 POTENTIAL.
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 210 POTENTIAL.
 FT DOMAIN 211 326 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 327 347 POTENTIAL.
 FT DOMAIN 348 350 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 351 371 POTENTIAL.
 FT DOMAIN 372 403 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 404 426 POTENTIAL.
 FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 452 POTENTIAL.

FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).
 FT VARIANT W -> R (in CMDJ).
 FT 292 /FTid=VAR_012192.
 FT 331 C -> R (in CMDJ).
 FT 331 /FTid=VAR_012193.
 FT 375 Missing (in CMDJ).
 FT 375 /FTid=VAR_012194.
 FT 376 Missing (in CMDJ).
 FT 376 /FTid=VAR_012195.
 FT 377 Missing (in CMDJ).
 FT 377 /FTid=VAR_012196.
 FT 380 P -> PA (in CMDJ).
 FT 380 /FTid=VAR_012197.
 FT 389 G -> R (in CMDJ).
 FT 389 /FTid=VAR_012198.
 FT 78 N -> S (in REF. 1).
 FT 78 CONFLICT
 SQ SEQUENCE 492 AA; 54240 MW; 44BFEE9089BDEC6B CRC64;
 Query Match 100.0%; Score 2527; DB 1; Length 492;
 Best Local Similarity 100.0%; Pred. No. 7.8e-195; Indels 0; Gaps 0;
 Matches 492; Conservative 0; Mismatches 0;
 QY 1 MVKFPALHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASGLAYSLMK 60
 DB 1 MVKFPALHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASGLAYSLMK 60
 QY 61 FTGPMSPDKVGLVFNKSKDRTKAVLCMVVAGIAAVFHTLIAYSDLYGIINKLHV 120
 DB 61 FTGPMSPDKVGLVFNKSKDRTKAVLCMVVAGIAAVFHTLIAYSDLYGIINKLHV 120
 QY 121 DESVGSKTRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
 DB 121 DESVGSKTRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
 QY 181 HSHLECREPLLIPLSLYNGALVRCITCLGYKNIHDIIPDRSGPELGGDATIKMLSF 240
 DB 181 HSHLECREPLLIPLSLYNGALVRCITCLGYKNIHDIIPDRSGPELGGDATIKMLSF 240
 QY 241 WPLALILATQIRISPVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGLTIRAVY 300
 DB 241 WPLALILATQIRISPVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGLTIRAVY 300
 QY 301 PAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVNFVTPNVSEKILIDIGVD 360
 DB 301 PAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVNFVTPNVSEKILIDIGVD 360
 QY 361 FAFAEICVVPRLRIFSPFPVTVRAHLTGWMTLTKTFLVAPSSVLRITVLIASLVLPY 420
 DB 361 FAFAEICVVPRLRIFSPFPVTVRAHLTGWMTLTKTFLVAPSSVLRITVLIASLVLPY 420
 QY 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKMENESATEGEDSAMTMPPTTE 480
 DB 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKMENESATEGEDSAMTMPPTTE 480
 QY 481 VTDIVEMRENE 492
 DB 481 VTDIVEMRENE 492
 RESULT 2
 ANKH_MOUSE
 ID ANKH_MOUSE STANDARD; PRT; 492 AA.
 AC Q9UHZ2; O35138; O35139;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progressive ankylosis protein (Fn54 protein).
 GN ANKH OR ANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A., AND VARIANT VAL-201.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 EX MEDLINE=20355194; PubMed=10894769;
 RA Ho A.M.; Johnson M.D.; Kingsley D.M.;
 RT "Role of the mouse ank gene in control of tissue calcification and
 RL arthritis.";
 RN Science 289:265-270 (2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Guo Y.; Hsu D.K.W.; Alberts G.F.; Feng S.-L.; Copeland N.G.;
 RA Gilbert D.J.; Jenkins N.A.; Peiffey K.A.; Winkles J.A.;
 RT "Molecular cloning and characterization of a mitogen-inducible gene
 RT differentially expressed in androgen-dependent and independent
 RT prostate carcinoma cell lines.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic
 CC pyrophosphate (Ppi), probably functioning as Ppi transporter.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, liver, spleen,
 CC lung, muscle, and kidney of adult animals. Strongly expressed in
 CC the developing articular cartilage of joints in the shoulder,
 CC elbow, wrist, and digits of the embryo.
 CC -!- DISEASE: Defects in ANKH are the cause of a generalized,
 CC progressive form of arthritis. In ank mice hydroxyapatite crystals
 CC develop in articular surfaces and synovial fluid leading to joint
 CC space narrowing, cartilage erosion, and formation of bony
 CC outgrowths or osteophytes that cause fusion and joint immobility
 CC and destruction.
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.
 CC
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 CC
 DR EMBL; AF274752; AAF88038.1; -;
 DR EMBL; AF001532; AAB65653.1; -;
 DR EMBL; AF001533; AAB65654.2; -;
 DR MGD; MGI:88023; ank.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR GO; GO:0030504; P:inorganic diphosphate transporter activity; IDA.
 DR GO; GO:0007626; P:locomotory behavior; IMP.
 DR GO; GO:0030500; P:regulation of bone mineralization; IMP.
 DR GO; GO:0001501; P:skeletal development; IMP.
 KW Transport; Phosphate transport; Transmembrane; Polymorphism.
 FT DOMAIN 1 85
 FT DOMAIN 86 106
 FT TRANSMEM 107 131
 FT DOMAIN 132 158
 FT TRANSMEM 159 179
 FT DOMAIN 180 199
 FT TRANSMEM 190 210
 FT DOMAIN 211 326
 FT TRANSMEM 327 347
 FT DOMAIN 348 350
 FT TRANSMEM 351 371
 FT DOMAIN 372 403
 FT TRANSMEM 404 426
 FT DOMAIN 427 429
 FT TRANSMEM 430 452
 FT DOMAIN 453 482
 FT VARIANT 201 201 A -> V (IN STRAIN C3H).
 SQ SEQUENCE 492 AA; 54297 MW; 8792B248C875688E CRC64;
 Query Match 99.0%; Score 2502; DB 1; Length 492;
 Best Local Similarity 98.4%; Pred. No. 7,9e-193;
 Matches 484; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVKFPALTHYNPLIRFLPLGTTINAIIDFGQALNRGIAAVKEDAVENLASYGLAYSLMK 60
 DB 1 MVKFPALTHYNPLIRFLPLGTTINAIIDFGQALNRGIAAVKEDAVENLASYGLAYSLMK 60
 QY 61 FTTGPMSPFNKVLVFNKSKDRKAVLCMVVAGAAIAVFFHTLIAYSDLYGYYINKLHHV 120
 DB 61 FTTGPMSPFNKVLVFNKSKDRKAVLCMVVAGAAIAVFFHTLIAYSDLYGYYINKLHHV 120
 QY 121 DESVGSKTRRAFLYLAAPFFMDAMAWTHAGILLKHKYSLVGCASISDVIAQVVFVAILL 180
 DB 121 DESVGSKTRRAFLYLAAPFFMDAMAWTHAGILLKHKYSLVGCASISDVIAQVVFVAILL 180
 QY 181 HSHLECREPLLIPIISLYMGALVRCVTTCLGYKYNHDIIDRSRGPGLGGDATIRKMLSF 240
 DB 181 HSHLECREPLLIPIISLYMGALVRCVTTCLGYKYNHDIIDRSRGPGLGGDATIRKMLSF 240
 QY 241 WPLALILATORISRPINLVNLFVSRDLGGSSAATEAVAILTATPYVGHMPYGLWTEIRAVY 300
 DB 241 WPLALILATORISRPINLVNLFVSRDLGGSSAATEAVAILTATPYVGHMPYGLWTEIRAVY 300
 QY 301 PAFDKNNPSNKLVSNTNTVTAHKKFTFCVMSLTLTLCFVNFMTNPNVSEKILIDIIGVD 360
 DB 301 PAFDKNNPSNKLVSNTNTVTAHKKFTFCVMSLTLTLCFVNFMTNPNVSEKILIDIIGVD 360
 QY 361 PAFDELCTVYPIRIFSFPPVPTVRAHLTGMLTKTFLAPSSVLRILVLTASLVLPY 420
 DB 361 PAFDELCTVYPIRIFSFPPVPTVRAHLTGMLTKTFLAPSSVLRILVLTASLVLPY 420
 QY 421 LGVHGATLGVGSLAGFVGESTWVAIAACYVYRKQKKMENESATEGDSAMTDPPTTE 480
 DB 421 LGVHGATLGVGSLAGFVGESTWVAIAACYVYRKQKKMENESATEGDSAMTDPPTTE 480
 QY 481 VTDIVEMREENE 492
 DB 481 VTDIVEMREENE 492
 RESULT 3
 ANKH RAT STANDARD; PRT; 492 AA.
 ID AC P58366;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN ANKH.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
 RA Miyashiro K.; Finnell R.H.; Eberwine J.;
 RT "Rat progressive ankylosis gene/termesin.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic
 CC pyrophosphate (Ppi), probably functioning as Ppi transporter (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane protein (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.
 CC
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 CC
 DR EMBL; AF393241; AAK73750.1; -;
 DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO:0019867; C:outer membrane; ISS.
 DR GO:0030504; F:inorganic diphosphate transporter activity; ISS.
 DR GO:0030500; P:regulation of bone mineralization; ISS.
 KW Transport; Phosphate transport; Transmembrane.
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 POTENTIAL.
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 132 152 POTENTIAL.
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 179 POTENTIAL.
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 210 POTENTIAL.
 FT DOMAIN 211 326 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 327 347 POTENTIAL.
 FT DOMAIN 348 350 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 351 371 POTENTIAL.
 FT DOMAIN 372 403 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 404 426 POTENTIAL.
 FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 452 POTENTIAL.
 FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 492 AA; 54264 MW; 99CAC276412ECOB CRC64;
 Query Match 98.5%; Score 2489; DB 1; Length 492;
 Best Local Similarity 97.8%; Pred. No. 8.6e-192;
 Matches 481; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MKVFPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60
 DB 1 MKVFPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60
 QY 61 FFTGPMDFKNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120
 DB 61 FFTGPMDFKNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120
 QY 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180
 DB 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180
 QY 181 HSHLECREPLIPILSLYMGALVRCCTTLCGLYYKNHDIIPDRSGPELGGDATIRKMLSF 240
 DB 181 HSHLECREPLIPILSLYMGALVRCCTTLCGLYYKNHDIIPDRSGPELGGDATIRKMLSF 240
 QY 241 WPLALILATORISRPVNLFSVLDGSSNAFAVAILTATVPVGHMPYCWLTETRAVY 300
 DB 241 WPLALILATORISRPVNLFSVLDGSSNAFAVAILTATVPVGHMPYCWLTETRAVY 300
 QY 301 PAFDKNPNKLVSTNTVTAAHIKKFTFCWALSLLTLCFVMTPTNVSEKILIDIIGVD 360
 DB 301 PAFDKNPNKLVSTNTVTAAHIKKFTFCWALSLLTLCFVMTPTNVSEKILIDIIGVD 360
 QY 361 FAPAEELCVVPLRIFSPFPVTVRAHLTGWLTKTFFVLAPSSVLIILVILASLVVLPY 420
 DB 361 FAPAEELCVVPLRIFSPFPVTVRAHLTGWLTKTFFVLAPSSVLIILVILASLVVLPY 420
 QY 421 LGVHGATLGVGSLLAGFVGEFTWVAIAACYVYRKQKKMENESATEGEDSAMDTPPTTE 480
 DB 421 LGVHGATLGVGSLLAGFVGEFTWVAIAACYVYRKQKKMENESATEGEDSAMDTPPTTE 480
 QY 481 VTDIVEMRENE 492
 DB 481 VTDIVEMRENE 492
 RESULT 4
 ANKH_XENLA
 ID ANKH_XENLA STANDARD; PRT; 492 AA.
 AC P58367;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progressive ankylosis protein homolog (ANK).
 GN ANKH.

OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21225282; PubMed=11326272;
 RA Nuenberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,
 RA Ritter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,
 RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,
 RA Braun H.-S., Laing N., Tinschert S.;
 RT "Heterozygous mutations in ANKH, the human ortholog of the mouse
 RT progressive ankylosis gene, result in craniometaphyseal dysplasia.";
 RL Nat. Genet. 28:37-41(2001).
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic
 CC pyrophosphate (Ppi), probably functioning as Ppi transporter (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.
 CC -----
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 CC -----
 CC EMBL: AJ302033; CAC40980.1; -;
 DR GO:0016021; C:integral to membrane; ISS.
 DR GO:0019867; C:outer membrane; ISS.
 DR GO:0030504; F:inorganic diphosphate transporter activity; ISS.
 DR GO:0030500; P:regulation of bone mineralization; ISS.
 KW Transport; Phosphate transport; Transmembrane.
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 POTENTIAL.
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 132 152 POTENTIAL.
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 179 POTENTIAL.
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 210 POTENTIAL.
 FT DOMAIN 211 327 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 328 348 POTENTIAL.
 FT DOMAIN 349 360 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 361 381 POTENTIAL.
 FT DOMAIN 382 403 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 404 426 POTENTIAL.
 FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 452 POTENTIAL.
 FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 492 AA; 53951 MW; 753214B87D7B5F23 CRC64;
 Query Match 91.7%; Score 2317; DB 1; Length 492;
 Best Local Similarity 90.2%; Pred. No. 5.1e-178;
 Matches 444; Conservative 25; Mismatches 23; Indels 0; Gaps 0;
 QY 1 MKVFPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60
 DB 1 MKVFPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60
 QY 61 FFTGPMDFKNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120
 DB 61 FFTGPMDFKNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120
 QY 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180
 DB 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180
 QY 181 HSHLECREPLIPILSLYMGALVRCCTTLCGLYYKNHDIIPDRSGPELGGDATIRKMLSF 240
 DB 181 HSHLECREPLIPILSLYMGALVRCCTTLCGLYYKNHDIIPDRSGPELGGDATIRKMLSF 240

QY 241 WPLALILATORISRPVNLVSRDLGGSSAATAVAAILTATYPVGHMPYGLTEIRAVY 300
 DB 241 WPLALILATORISRPVNLVSRDLGGSSAATAVAAILTATYPVGHMPYGLTEIRAVY 300
 QY 301 PAFDKNSPKLVSTNTVTAHKKFTVCWALSILTLCTVFMFTPNVSEKILDIIGVB 360
 DB 301 PAFDKNSPKLVSTNTVTAHKKFTVCWALSILTLCTVFMFTPNVSEKILDIIGVB 360
 QY 361 FAFALCVVPLRIFSPFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRIVLIIASVLPY 420
 DB 361 FAFALCVVPLRIFSPFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRIVLIIASVLPY 420
 QY 421 LGVHGATLGVSLLAGFVGSSTWVAIAACVYRKQKKKNESATEGEDSAMTDPTEE 480
 DB 421 LGVHGATLGVSLLAGFVGSSTWVAIAACVYRKQKKKNESATEGEDSAMTDPTEE 480
 QY 481 VTDIVEMRENE 492
 DB 481 LTDIVEIKEDGE 492

RESULT 5
 ANKH BRARE
 ID ANKH BRARE STANDARD; PRT; 501 AA.
 AC P58368;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progressive ankylosis protein homolog (ANK).
 GN ANKH.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteiophysii; Cypiniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21225282; PubMed=11326272;
 RA Nuerberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,
 RA Ritter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,
 RA Goldblatt J., Borochowitz Z.U., Korzot D., Westermann F., Mundlos S.,
 RA Braun H.-S., Laing N., Tinschert S.;
 RT "Heterozygous mutations in ANKH, the human ortholog of the mouse
 RT progressive ankylosis gene, result in cranioetaphyseal dysplasia."
 RL Nat. Genet. 28:37-41(2001).
 CC -!- FUNCTION: regulates intra- and extracellular levels of inorganic
 CC pyrophosphate (PPi), probably functioning as Ppi transporter (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.

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 ENBL; AJ302035; CAC40781.1;
 DR GO; GO:0016021; C:integral to membrane; ISS.
 DR GO; GO:0019857; C:outer membrane; ISS.
 DR GO; GO:0005315; F:inorganic phosphate transporter activity; ISS.
 DR GO; GO:0030500; P:regulation of bone mineralization; ISS.
 KW Transport; Phosphate transport; Transmembrane.
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 POTENTIAL.
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 132 152 POTENTIAL.
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 179 POTENTIAL.
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 190 210 POTENTIAL.
 FT DOMAIN 211 327 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 328 348 POTENTIAL.
 FT DOMAIN 349 362 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 363 383 POTENTIAL.
 FT DOMAIN 384 403 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 404 426 POTENTIAL.
 FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 452 POTENTIAL.
 FT DOMAIN 453 501 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 501 AA; 55415 MW; E2A4F63628717CB4 CRC64;

Query Match 85.4%; Score 2158.5; DB 1; Length 501;
 Best Local Similarity 83.0%; Pred. No. 2.5e-165;
 Matches 411; Conservative 45; Mismatches 36; Indels 3; Gaps 2;

QY 1 MKKPPALTHWPLRIFLPLGINTIAIDFGEOALNRGIAAKEDAVEMLASYGILSLMK 60
 DB 1 MKKPPALTHWPLRIFLPLGINTIAIDFGEOALNRGIAAKEDAVEMLASYGILSLMK 60
 QY 61 FFTGPMDSDFKNVGLVFNVSKRDRTKAVLCMVVAGATAAVERHTLIAYSDLGYYINKLHHV 120
 DB 61 FFTGPMDSDFKNVGLVFNVSKRDRTKAVLCMVVAGATAAVERHTLIAYSDLGYYINKLHHV 120
 QY 121 DESVGSKTRRAFLYLAAPFPMDAMWATHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
 DB 121 DESVGSKTRRAFLYLAAPFPMDAMWATHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
 QY 181 HSHLECEPPLIPILSLYMGALVRCCTLCIGYKYNHDIIPDRSGPGLGDDATIRKMLSF 240
 DB 181 HSHLECEPPLIPILSLYMGALVRCCTLCIGYKYNHDIIPDRSGPGLGDDATIRKMLSF 240
 QY 241 WPLALILATORISRPVNLVSRDLGGSSAATAVAAILTATYPVGHMPYGLTEIRAVY 300
 DB 241 WPLALILATORISRPVNLVSRDLGGSSAATAVAAILTATYPVGHMPYGLTEIRAVY 300
 QY 301 PAFDKNSPKLVSTNTVTAHKKFTVCWALSILTLCTVFMFTPNVSEKILDIIGVB 360
 DB 301 PAFDKNSPKLVSTNTVTAHKKFTVCWALSILTLCTVFMFTPNVSEKILDIIGVB 360
 QY 361 FAFALCVVPLRIFSPFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRIVLIIASVLPY 420
 DB 361 FAFALCVVPLRIFSPFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRIVLIIASVLPY 420
 QY 421 LGVHGATLGVSLLAGFVGSSTWVAIAACVYRKQKKKNESATEGEDSAMTDPTEE 477
 DB 421 LGVHGATLGVSLLAGFVGSSTWVAIAACVYRKQKKKNESATEGEDSAMTDPTEE 477
 QY 478 TEEVTDIVEMRENE 492
 DB 481 RGRWDDIVELREDE 495

RESULT 6
 ANKH TETNG
 ID ANKH TETNG STANDARD; PRT; 355 AA.
 AC P58369;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progressive ankylosis protein homolog (ANK) (Fragment).
 GN ANKH.
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle.
 RX MEDLINE=21225282; PubMed=11326272;
 RA Nuerberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,

RA Ritter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,
RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,
RA Braun H.-S., Laing N., Tinschert S.;
RT "Heterozygous mutations in ANKH, the human ortholog of the mouse
progressive ankylosis gene, result in cranioetaphyseal dysplasia.";
RL Nat. Genet. 28:37-41(2001).
CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic
pyrophosphate (PPi), probably functioning as Ppi transporter (By
similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.
CC
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CC
CC EMBL; AJ302034; CAC40964.1; -; 09A70DCFP80F1B5C CRC64;
DR TRANSPORT; Phosphate transport; Transmembrane.
FT NON TER 1 1
FT TRANSMEM 20 - 40 POTENTIAL.
FT TRANSMEM 66 86 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 296 316 POTENTIAL.
FT TRANSMEM 331 351 POTENTIAL.
FT NON TER 355
SQ SEQUENCE 355 AA; 39336 MW; 09A70DCFP80F1B5C CRC64;

Query Match 60.5%; Score 1528.5; DB 1; Length 355;
Best Local Similarity 82.0%; Pred. No. 4.7e-115;
Matches 292; Conservative 31; Mismatches 32; Indels 1; Gaps 1;

QY 67 SDFKNGVLVFNYSKEDRTKAYLCMVVAGIAAFTLTIAYSDLGYYIINKLHVDES VGS 126
Db 1 SDFKNGVLVFNYSKEDRKAMFLITAGTAFVLIHIIAYTDLGYIINKLHVDES VGG 60

QY 127 KTRAFLYLAFFPPNDANAWTHAGILKHKYSLVGCASDSVIAQVFAILLHSHLEC 186
Db 61 KTRAFLYLAFFPPDLALAWHAGILKHKYSLVGCASDSVIAQVFAILLHSHLEC 120

QY 187 REPLIPILSYMGALVCTTCLGYGKNIHDIIPDRSGPGLGGDATIRKMLSFWWPLAL 246
Db 121 ABPLIPILSYMGALVFTVGLGYGKNIHDIIPDRSGPGLGGDATIRKMLSFWWPLAL 180

QY 247 ILATORISRPVNLVFSRDLGSSAATEAVAILTATYVGHMPYGLWTEIRATYPAFDKN 306
Db 181 ILATORISRPVNLVFSRDLGSSAATEAVAILTATYVGHMPYGLWTEIRATYPAFDKN 240

QY 307 NPSNKLVSNTVTAAHIKKFTFCVCMALSLTLCFVMEFTPNVSEKILIDIIIGVDFAFEL 366
Db 241 NPSNK-INASSPVTKSHIKKFTFCCLALSMLCFVLFVTPHSEKILVDVIGVDYAFEL 299

QY 367 CVVPLRIISFPVPTVRAHLTGWMLTKKTFVLPAPSSVLRITVLIASLVLPYLK 422
Db 300 CVVPLRIISFPVPTVRAHLTAWLTKKTFVLPAPSSVLRITVLIASLVLPYLK 355

RESULT 7
LACY_KLEOX
ID LACY_KLEOX STANDARD; PRT; 416 AA.
AC P18617;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactose permease (Lactose-proton symport).
GN LACY.
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M5a1;
RX MEDLINE=89050993; PubMed=3056524;
RA McMorrow J., Chin D.T., Fiebig K., Pierce J.L., Wilson D.M.,
RA Reeve E.C.R., Wilson T.H.;
RT "The lactose carrier of Klebsiella pneumoniae M5a1; the physiology of
Biochim. Biophys. Acta 945:315-323(1988).
RL -!- FUNCTION: RESPONSIBLE FOR TRANSPORT OF A PROTON (SYMPORT SYSTEM).
CC -!- CELL, WITH THE CONCOMITANT IMPORT OF A PROTON (SYMPORT SYSTEM).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE LACY/RAPB FAMILY OF PERMEASES.
CC
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CC
CC EMBL; X14154; CAA32366.1; -;
DR PIR; C24925; C24925.
DR InterPro; IPR000576; Lacy_symport.
DR InterPro; IPR007114; MFS.
DR Pfam; PF01306; Lacy_symp; 1.
DR PRINTS; PRO0174; LACYSYMPORT.
DR TIGRFAMs; TIGR00882; 2A0105; 1.
DR PROSITE; PS00896; LACY_1; 1.
DR PROSITE; PS00897; LACY_2; 1.
DR PROSITE; PS00850; MFS; 1.
KW Transport; Sugar transport; Symport; Inner membrane; Transmembrane.
FT DOMAIN 1 13
FT TRANSMEM 14 34
FT DOMAIN 35 50
FT TRANSMEM 51 71
FT DOMAIN 72 80
FT TRANSMEM 81 101
FT DOMAIN 102 107
FT TRANSMEM 108 130
FT DOMAIN 131 149
FT TRANSMEM 150 170
FT DOMAIN 171 172
FT TRANSMEM 173 193
FT DOMAIN 194 223
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FT DOMAIN 289 316
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FT DOMAIN 340 353
FT TRANSMEM 354 374
FT DOMAIN 375 384
FT TRANSMEM 385 405
FT DOMAIN 406 416
SQ SEQUENCE 416 AA; 46220 MW; A37D8BA4C38C467B CRC64;

Query Match 4.5%; Score 114; DB 1; Length 416;
Best Local Similarity 22.7%; Pred. No. 0.099;
Matches 95; Conservative 50; Mismatches 145; Indels 128; Gaps 22;

QY 132 FYLAAFPMDAMW-THAGILKHKYSLVGCASISDVIAQVFAILL-LSHSHLEC 186
Db 26 FMSAYFFPPF-VMLAEVNHLTETGIVFSCISLFAIFQVFLGSLDKLGRKLLW 83

QY 187 REPLLI-----PIL--SLVMGALVCTTCLGYGKNIHDIIPDRSGP----- 226
Db 84 TITILLFAPPIFVPSFLQNNINAGALVG-----GVYLGIVFSSRSRGAVEAYTE 135

Query Match 4.5%; Score 113.5; DB 1; Length 556;
Best Local Similarity 19.5%; Pred. No. 0.15; Mismatches 141; Indels 169; Gaps 21;
Matches 94; Conservative 78;

QY 227 -----ELG-----GDA-----TIRKMLSFWP--LALILATQIRSPIV 258
DB 136 RVSRANREYKVRVSGVGCWALCASITGIILSDPNITFIWASGFALILG-----V 187
QY 259 NLFVSRDLGSSAAT-----EAVAILTATYPVGHMPYCW-----LTERAVYPAFDK 305
DB 188 LLWVSKPSSNSAEVIDALGANRQAFNRTRAA-ELFRMPRWGFIIVGVASVYDFDQ 246
QY 306 N-NPSNKLVTSTNTVTAHHKKTFTVCMALSLTLCFVWFTPNVSEKI----- 352
DB 247 QFANFFKGFSSPQSGT-----EVFGVTTGGELLNALIMFCAPAIINRIGAKNALLIAGL 302
QY 353 --LIDIIIGVDFAFELCVVPRIRIFSFPPVTVRAHITGMLTKTFLVAPSSVLRII- 409
DB 303 IMSVRLGSSFATSVEVILKMLHMFELPL-----LVGTKEYISSAFKGLSATLFLIG 358
QY 410 -----VLIASVLVLPY--LVHGTATLVGSLLAGFV-----GESTWVAIAA 448
DB 359 FNLSKQLSSVLSAWVGMYDVGPHQAYLILGCTILSFTVISLFLTKGSKTLLPATA 416

RESULT 8
NUZM_PODAN
ID NUZM_PODAN STANDARD; PRT; 556 AA.
AC P15578;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
GN ND2.
OS Podospora anserina.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
OX NCBI_TaxID=5145;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=s, and A;
RX MEDLINE=89125610; PubMed=2975708;
RA Cummings D.J., Domenico J.M.;
RT "Sequence analysis of mitochondrial DNA from Podospora anserina.
RT Pervasiveness of a class I intron in three separate genes.";
RL J. Mol. Biol. 204:815-839(1988).
RN [2]
RP COMPLETE GENOME.
RC STRAIN=s;
RX MEDLINE=90291512; PubMed=2357736;
RA Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
RT "The complete DNA sequence of the mitochondrial genome of Podospora
RT anserina.";
RL Curr. Genet. 17:375-402(1990).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC -----
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CC -----
CC EMBL; X55026; CAA38765.1; -;
DR EMBL; X14485; CAA32646.1; -;
DR PIR; S02154; S02154.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 556 AA; 62554 MW; 5613ACB0D2324BAF CRC64;

QY 13 LIRFL-----VPLGITNIAIDFGEQALN-----RGIAAYKEDAVEMLA-----SYG 53
DB 177 LIVFLLGGLSSCFILLGTSLLYINSISDVKDGADMPALTSWYKSY 236
QY 54 LAYSIMKFTGPMSPDKNVGLVFNKSRDRTKAVLCMVVAGAAVAFHFLIAYSDLYVI 113
DB 237 LNFALLVFIGEL--FKVSAAPFHWSPDVYDAI-----PTIVTFVAILIAKISIFEL 288
QY 114 INKLHVDESVSQSKTRAFYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQV 173
DB 289 LELAVYHTNN-----YLSEF-----SWTVL-LLISLSFLSIIGTVV---GLTQF 327
QY 174 VFVAILHSHLECRPLILPILSLYMGALVRCCTTCLGYKNIHDIIPDSGPELGSDAT 233
DB 328 RIKRLIAYSTIS-----HVGFIILLALSGC-----S 352
QY 234 IRKMLSFWMPLALILATQIRSPIVNLVFSRDLGSSAATEAVAILTATYPVGHMPYGL 293
DB 353 IESTQAFIFVL-----IQYSISNLV-----FIIIT---IGFSLYGYI 388
QY 294 TEIRAVYPAFDKNNPSNKLVTSTNTVTAHHKKTFTVCMALSLTLCFVWFTPNVSEKIL 353
DB 389 TTNKEYKDLLDKNSPIQVIS-----QLKGYFYINFLSLSLAITIF----- 430
QY 354 IDIIG-----VDPAFELCVVPLRIFSFPPVTVRAHITG-----WMLTKKTFTVLAP- 402
DB 431 -SFVGIPPLVGP-FAKQWLSAALDNGY-IFLTLLAILTSVIGAVVYLAIIKKIFFYLPD 487
QY 403 -----SSVRIIVLIASVLVLPYLGHGATLVGVS 432
DB 488 HSINPSIGEFLEFKKGLIFEAGDFKGRITLISPPSITISITLVILLFIEMKWEKLSMGT 547
QY 433 LL 434
DB 548 IL 549

RESULT 9
COX1_BACSU
ID -COX1_BACSU STANDARD; PRT; 622 AA.
AC P24010; O34467;
DT 01-MAR-1992 (Rel. 21, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Cytochrome aa3
DE subunit 1) (Caa-3605 subunit 1) (Oxidase aa(3) subunit 1).
GN CTAD OR BSU14900.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=91146590; PubMed=1847686;
RA Saraste M., Metsio T., Nakari T., Jalli T., Laureaus M.,
RA van der Oost J.;
RT "The Bacillus subtilis cytochrome-c oxidase. Variations on a
RT conserved protein theme.";
RL Eur. J. Biochem. 195:517-525(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Bertero M., Presecan E., Richou A., Banchin A.;
RT "Bacillus subtilis chromosomal region downstream nprA.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerston I.F., Cummings N.D., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Erington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haelech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwolltek S., Prescott A.M.,
RA Presecan E., Fujic P., Putnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche M., Sadai Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipet A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "the complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B. THIS CYTOCHROME C OXIDASE SHOWS PROTON PUMP ACTIVITY
CC ACROSS THE MEMBRANE IN ADDITION TO THE ELECTRON TRANSFER.
CC -!- CATALYTIC ACTIVITY: 4 ferredoxin + 2 H⁺ + O₂ = 4 ferredoxin + H₂O.
CC -!- COFACTOR: Two heme groups and copper B.
CC -!- PATHWAY: Respiratory chain; terminal step.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 14
CC POTENTIAL TRANSMEMBRANE DOMAINS.
CC -!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
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CC -----
DR EMBL; X54140; CAA38077.1; -;
DR EMBL; Z98682; CAB11343.1; -;
DR EMBL; Z99111; CAB13363.1; -;
DR PIR; B69609; E69609.
DR HSP; P18401; 1FFT.
DR Subtilist; BG10216; ctad.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
KW Hydrogen ion transport; Complete proteome.
FT DOMAIN 1 27
FT TRANSMEM 28 46
FT DOMAIN 47 68
FT TRANSMEM 69 88
FT DOMAIN 89 110
FT TRANSMEM 111 128
FT TRANSMEM 129 159
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FT TRANSMEM 13

PT2A ARATH STANDARD; PRT; 610 AA.
 AC P46031.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Peptide transporter PTR2-A.
 GN PTR2-A OR PTR2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=95003713; PubMed=7919993;
 RA Steiner H., Song W., Naider F., Becker J.M., Stacey G.;
 RT "An Arabidopsis peptide transporter is a member of a new class of
 membrane transport proteins."
 RL Plant Cell 6:1289-1299(1994).
 CC -!- FUNCTION: Peptide transport.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the PTR2 family of transporters.
 CC -----
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 CC -----
 CC EMBL; U01171; AA53173.1;
 DR InterPro; IPR000109; PTR2.
 DR Pfam; PF00854; PTR2; 1.
 DR PROSITE; PS01022; PTR2_1; 1.
 DR PROSITE; PS01023; PTR2_2; 1.
 KW Peptide transport; Transmembrane.
 FT TRANSMEM 71 91
 FT TRANSMEM 131 151
 FT TRANSMEM 161 181
 FT TRANSMEM 187 207
 FT TRANSMEM 247 267
 FT TRANSMEM 273 293
 FT TRANSMEM 300 320
 FT TRANSMEM 400 420
 FT TRANSMEM 430 450
 FT TRANSMEM 475 495
 FT TRANSMEM 511 531
 FT TRANSMEM 541 561
 SQ SEQUENCE 610 AA; 67518 MW; 6AE94D9E54DDA2D6 CRC64;
 Query Match 4.3%; Score 109.5; DB 1; Length 610;
 Best Local Similarity 18.9%; Pred No. 0.35;
 Matches 110; Conservative 93; Mismatches 172; Indels 207; Gaps 29;
 QY 7 LTHYPLRIFLVPLGLTINIAIDFGQALNR-----GI-----AAVKE--DAV 46
 DB 132 LSNFFTFWCYVTPVGAALIA-----DQFLGRYNTIVCSAVIYFIIILTCTAIPSDVIDAG 187
 QY 47 EMLASGLAYSLMKFTGPDSDFKNGLV-----FVNSKDRDKAVLCMVAGAI 96
 DB 188 KSMGGFVWSLIILIGLTGIGK-----SNVSPUMAEQLPKIPPYVTKNGSKVIVDPVPT 242
 QY 97 AAVFHTLIAYSDLGYYIKLHVDSEVGS-----KTRAFLYLAAPFMDAMAWT 147
 DB 243 -----TSRAYM-IFYWTIN-----VGSLSVLATTSLESTKGFVYALLPL----- 281
 QY 148 HAGILLKHKYSFLVGCASISDVIAQVFAVILLHSHLECRBELLPIILSYNGALVRCIT 207
 DB 282 -----CVFVIPL-----ILAVSKTAFTSTLPPFVPSLFV--LVKCSS 317
 QY 208 LCLGYKYNTHDIIPDRSGPELGGDATIRKVLFWFPLALILATQIRSPVNLVFSRDLG 267

DB 318 LLL--KTNL-----ISKLNH-----LALLLRYVKQWDLFD--ELK 354
 QY 268 GSSAATEAVAILTATYPPGHMYPGMLTETRAVYPAPFDKNPSNKLIVSTNTVTAHI--- 324
 DB 355 RALRACKTFLF---YPIVWCYQGT-----NNLSIQAGQWGTGNVSD 395
 QY 325 --KKFTFCMALSLTLC-----FVMTWPNVSKILIDI-IGVDFP----- 362
 DB 396 LFQAEDSIALIIFIPICDNIIYPLLRKYNIPKPIRLITLGFMFATASMIYAAVLOAKIY 455
 QY 363 -----PAELCV-----VPLRTFSPPEVPVTVRAHLTGMLTKLTKTFVLAPSSV 405
 DB 456 QRGPCVANFTDTCVSDNDISVWIIQIPAYVLIAS---EIFASITG---LEFAFTKAPSM 508
 QY 406 LRII-----VLIASIVLPYLVGHGATLGVGSLLAGFVGESTWVAIAAY 450
 DB 509 KSIITALFLFTNAFGAIIISICISSTAVNPKLTMWTGTIAVTAFIAG-----IMFWVCF 561
 QY 451 VYRKQKKWENESATGEDSANTMDPPTTEEVTDIVEMRENE 492
 DB 562 HHYDAMEEQNQLEFKRND-AUTKKDVEKEVHDSYMADESQ 602
 RESULT 11
 EXUT_BACSU STANDARD; PRT; 422 AA.
 AC 034456;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hexuronic transporter.
 GN EXUT OR BSU12360.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98240225; PubMed=9579062;
 RA Rivolta C., Soldo B., Lazarevic V., Joris B., Mavel C., Karamata D.;
 RT "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
 RT containing a putative 12.3 kb operon involved in hexuronate catabolism
 RT and a perfectly symmetrical hypothetical catabolite-responsive
 RT element."
 RL Microbiology 144:877-884(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerthof A., Ehrlich S.D., Emerson P.T.,
 RA Denizot F., Devine K.M., Dusterhoft A., Fajri E., Foulger D.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Galloway N.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 RA Gim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
 RA Saco T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzengger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: Aldonhexuronate transport system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the phthalate permease family.
CC
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CC
CC EMBL; AF015825; AAC46332.1; -.
CC EXBL; Z98110; CAB13093.1; -.
CC PIR; A69853; A69853.
CC Subtilisin; BG13210; exuT.
DR InterPro; IPR004744; Dgal_transporter.
DR InterPro; IPR007114; MFS.
DR Pfam; PF00083; sugar_tr_1.
DR TIGRfam; TIGR00893; 2A0114; 1.
DR PROSITE; PS50850; MFS; 1. Complete proteome.
KW Transmembrane; Transport; Complete proteome.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 45 65 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 219 239 POTENTIAL.
FT TRANSMEM 256 276 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
FT TRANSMEM 321 341 POTENTIAL.
FT TRANSMEM 356 376 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
SQ SEQUENCE 422 AA; 45313 MW; C2E291AF347F7EDD CRC64;

Query Match 4.2%; Score 107; DB 1; Length 422;
Best Local Similarity 20.7%; Pred. No. 0.37;
Matches 88; Conservative 62; Mismatches 125; Indels 150; Gaps 22;

QY 81 RDRTKAVLCMVVAGIAAFAVHTLIAYSDLGYYIINKLHHVDESVGSKTRRAFLYLAAFPF 140
DB 4 KKLPLVILFLAGVI-----NYLD-----RSALSIAA-PF 33

QY 141 MD---AMAWTHAGILLKH-----KYGFLVGCASISDVIAQVVFVAILLHSHLECREPLL 191
DB 34 IQDDLTLSATQMLGTFSSFSFGYAFNPLGFGVADRYGAKLTLFVAVV----- 81

QY 192 IPILSLYMGALVRCITLCGLGYVK--NTHDIIPDRSGPELGGDATIRKMLSPWPLALILA 249
DB 82 --VMSLFGAV-----ALAFGVSLIILIRLPGMEGEL---SATINKVNNWEP-----P 127

QY 250 TOR-----ISRPIVNLFP-VSRDLGGSSAATEAVAILTAY---PVGHMP 289
DB 128 TORASVIGVNTSGTPLGGAISGPIVGMIAVAFSNKVSFVLIMITGLIWAIVLWPKFVKPKP 187
QY 290 YGWLTEIRAVYPAPDKXNPSNKLAVSTNTVTAHKKFT-----FVCMALSLTL-CFVMPF 344
DB 188 QETIKEAPAIKA---ETSPGKEKIPLT-----FYLKOKTVLFTAFAPFAFYNYLFFFLTW 239
QY 345 TPNVSEKILIDIIGVDFAEALCVVPLAIFSFVFPVPTVRAHLTGWLM----- 392
DB 239 FPS-----YLVBERG-----LSVESMSVITVIP-----WILGIGLAAGGFVS 276
QY 393 --TLKKTF---VLAPSSVLRIVLIASLVLPILGVGHGATLGVCSILLAGFVGSTWVIA 447

DB 277 DYVYKTKARKGVLFSRKQVLTCLFSSAVLIGFAG-----LVATTAGAVTLVALS 326
QY 448 ACYVY 452
DB 327 VFFLY 331

RESULT 12
LAT2 RAT
ID LAT2 RAT STANDARD; PRT; 533 AA.
AC Q9WVR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Large neutral amino acids transporter small subunit 2 (L-type amino
DE acid transporter 2).
GN SLC7A8 OR LAT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=99321902; PubMed=10391916;
RA Segawa H., Fukasawa Y., Miyamoto K., Takeda E., Endou H., Kanai Y.;
RT "Identification and functional characterization of a Na+-independent
RT neutral amino acid transporter with broad substrate selectivity";
RL J. Biol. Chem. 274:19745-19751(1999).
CC -!- FUNCTION: Sodium-independent, high-affinity transport of large
CC neutral amino acids. Has higher affinity for L-phenylalanine than
CC lat1. L-alanine is transported at physiological concentrations.
CC Plays a role in basolateral (re)absorption of neutral amino acids.
CC -!- SUBUNIT: Disulfide-linked heterodimer with the amino acid
CC transport protein SLC3A2/4F2hc.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
CC PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAT)
CC SUBFAMILY.
CC
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CC EMBL; AB024400; BAA82517.1; -.
DR InterPro; IPR002393; AA/rel_permease1.
DR InterPro; IPR004760; L_AA_transporter.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; aa_permeases; 1.
DR TIGRfam; TIGR00911; 2A0308; 1.
KW Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 114 134 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
FT TRANSMEM 190 210 POTENTIAL.
FT TRANSMEM 232 252 POTENTIAL.
FT TRANSMEM 269 289 POTENTIAL.
FT TRANSMEM 311 331 POTENTIAL.
FT TRANSMEM 363 383 POTENTIAL.
FT TRANSMEM 399 409 POTENTIAL.
FT TRANSMEM 423 443 POTENTIAL.
FT TRANSMEM 448 468 POTENTIAL.
SQ SEQUENCE 533 AA; 58190 MW; 99479DB60DA69DF0 CRC64;

Query Match 4.2%; Score 107; DB 1; Length 533;
Best Local Similarity 20.7%; Pred. No. 0.48;
Matches 114; Conservative 78; Mismatches 192; Indels 168; Gaps 30;

QY 37 GIAAVKEDAVEMLASYGAYLSM---KEFTGMSDFKNGVLVFNYSKDRTKAVLCMWVA 93
 Db 34 GVALKKE--IGLVACGIIVNGIISGIFVSPKGVLENAGSVGL-----ALIVMIVT 83
 QY 94 GAIAAVFHTLAYSGLGYIINKLHVDESIG--SKTRRAFLYLAAFPFMDAMAWTHAGI 151
 Db 84 GVITRAV--GALCYAELGVTI-----PKSGDISYVKDIFGGLAGP-----LRLW--IAV 128
 QY 152 LLKHYSFLVGCASISDVIAQVVF-----VAILHSHLECRE----- 188
 Db 129 LIVIPTNQAVIALTFNSVVLQPLPTCPPEPSGLRLAAICLLLLTWNCSSVRWATRVQ 188
 QY 189 -----PLLIIPILSYMGALVRCVCTLCIGYV-----KNHIDILIPDRSGPELGGDATIKM 237
 Db 189 DIFTAGKLLALAIITINGVW---QICKGEFFWLEPRNAFENFOR---PDIGLVALAFLQ 241
 QY 238 LSF---WMLALILATORISRPVNL-----FVSRDLGGSSA-----AT 273
 Db 242 GSFAVGGWNF--LNYVTEELVDPYKNLPRAIFISPLVTFVVFANIAVVTAMSPQELLAS 300
 QY 274 EAVAILTATYPVGHMPYQWLTIRAVYAPFKNPNKLVST-----NTVT 320
 Db 301 NAVAVTFGEKLLGVN--AWIMPIVSALSTFGGVNGS--LFTSSRLFFAGAREGHLPSVLA 356
 QY 321 AAHIKKFT-----FVCMALSITLCFVMFWTPNVSEKILIDIIG--VDPAPAEELCVV--- 369
 Db 357 MHVRCFTPIPALFTCLSTLLMLVTSDMYT-----LINYVGFVNLVFGVTVAGQIV 409
 QY 370 -----PLRISFPFPVTVRAHLLTGMVMTLTKTFLVAPSVLRRIIVLIASLVLP 419
 Db 410 LEWKKFPDIPRKIKSLLFPI-----IYLLFWAFL--IFSLWSEFPVCGIGLAIMLTGVP 462
 QY 420 --YLVGHGATLVGSLAGFVGESTMVALAACVYVYRKQKKVNESEATGEGDSAMTDMPP 477
 Db 463 VYFLGVYQW--HKPKCFNDFIESLTVSQKCVVYVQ-----EGDSGTG----- 505
 QY 478 TBEVTDIVEMRE 489
 Db 506 -ETIDVVEQHK 516

RESULT 13
 YB77_METJA
 ID YB77_METJA STANDARD; PRT; 334 AA.
 AC Q58578;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ1177.
 GN MJ1177.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrow P.W., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadown P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii";
 RL Science 273:1058-1073 (1996).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.

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 CC -----
 CC EMBL; U67559; AAB99180.1; -.
 DR PIR; A64447; A64447.
 DR TIGR; MJ1177; -.
 DR InterPro; IPR002549; UPF0118.
 DR Pfam; PF01594; UPF0118; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 13 33 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT TRANSMEM 259 279 POTENTIAL.
 FT TRANSMEM 293 313 POTENTIAL.
 SQ SEQUENCE 334 AA; 38445 MW; FD7429A229130200 CRC64;
 Query Match 4.2%; Score 106; DB 1; Length 334;
 Best Local Similarity 19.3%; Pred. No. 0.34;
 Matches 74; Conservative 71; Mismatches 111; Indels 128; Gaps 19;
 QY 133 LVLAAPFMDAMAWTHAGI-----LLKHYSFLVGCASIS-----DVIAQV 174
 Db 22 LYI--IWFFDVLAYSAPAYMALPVNIRKFNKNTISAGLAISIVILPMTITIYALLT 80
 QY 175 FVAILHSHLECREPLILPILSY-----MGALVRCVCTLCIGYVKN--IHDIIPDRSGPELG 229
 Db 81 FMEIILSFNTKSTIEPVINEILSYNSFMLEIRINEQIIAKYIDEIFKLVVSQFSKIID 140
 QY 230 GDATIRKMSFWWPLALILATORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMP 289
 Db 141 VGVLIVKVI-----WVL-----FTFFPLRD--GDKXNLIISFVPEY----- 177
 QY 290 YGWLTEIRAVYAPFADKNNFNSKLVSTNTVTAHKKFTFVCMALSLTLCFVNFVTPNVS 349
 Db 178 ---XKKRIYLSYLDHSDYKNLFS-----LGMMVVIISIAIYFFLIHDTYKA 211
 QY 350 EKILIDIIGVDFAFELCVVPLRIFSPFPVTVRAHLLTGMVMTL-----KK 396
 Db 212 --IGYLILGV--PYAELFAITGIFALLPI-----LGMMVVIISIAIYFFLIHDTYKA 260
 QY 397 TFV-----LAPSSVLR-----IIVLIASLVLPYLVGHGATLVGSLLA 435
 Db 261 VFMYIGELFSLTAPDFVIRPVLVKEVDHPVLVVIAPLWAPLSLGLSG--PAIGPLVV 318
 QY 436 GFVGESTMVAIAACVYRKQKKM 459
 Db 319 G-----ALNAPYLAKYRDKKI 334

RESULT 14
 LSGI_HABIN
 ID LSGI_HABIN STANDARD; PRT; 401 AA.
 AC P71399; Q48210;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lsg locus putative protein 1.
 GN H1700.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A2;
 RA McLaughlin R., Abu Kwaik Y., Young R., Spinola S., Apicella M.;

"Characterization and sequence of the *isg* locus from Haemophilus influenzae";
Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
[2]

RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=9535630; PubMed=754280;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierulff A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudke D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.J., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.W., Smith H.O.,
RA Venter J.C.;
RI "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the polysaccharide synthase family.
CC H10867/H11700 SUBFAMILY.

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DR EMBL; M94855; AAC24978.1; -;
DR EMBL; U32842; AAC23346.1; ALT_INIT.
DR PIR; H64175; H64175.
DR TIGR; H11700; -;
DR InterPro; IPR002797; Polysacc_synt.
DR Pfam; F01943; Polysacc_synt; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 26 POTENTIAL.
FT TRANSMEM 36 56 POTENTIAL.
FT TRANSMEM 132 107 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 162 182 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 237 257 POTENTIAL.
FT TRANSMEM 282 302 POTENTIAL.
FT TRANSMEM 320 340 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 374 394 POTENTIAL.
FT TRANSMEM 249 249 V -> I (IN REF. 1).
FT CONFLICT 276 276 V -> I (IN REF. 1).
FT CONFLICT 358 358 I -> V (IN REF. 1).
SQ SEQUENCE 401 AA; 45944 MW; FE2E7B02747B0874 CRC64;

Query Match 4.2%; Score 105; DB 1; Length 401;
Best Local Similarity 18.8%; Pred. No. 0.5;
Matches 75; Conservative 62; Mismatches 133; Indels 128; Gaps 17;

QY 106 YSDLOYIYINKLHVDSVGSKTRAFILYLAAPFMDAMWTHAGILKHKYSP----- 159
Db EMBL; Y12842; AAC23346.1; ALT_INIT.
37 YGSLSY-----QTFLSL-----FLIVSLTQEGASIRYFYFGKSLN 75
QY 160 -----LVGC-----ASISDVIAQVVFVAILLHSHLECKREP--- 189
Db LVVNTGYATTIGSIIIGCWIAQSEILFYAALLSIFQSLNVLQ-----SVRCQCKAWS 132
QY 190 -LLIFILSYGALVRCITCLGYKYNTHDIPDRSGPELGGDATI-----RK----- 236
Db YAFIOFSLTGTGAVF--VALLLEYQN--DLVEKRILAILLSNLVWFFSYFLRKSTTS 189
QY 237 -----MLSEWPLALILATORISRPVNLV-----SRDLGSSAATAEVA 277
Db KXQKQHYQSALFYILGFLPLILHYAFFLKQLDRIFVHKPSDTGLGYANGAQLAL 248

QY 278 ILTATYVGHMPYGMWLTETRAVYPAFDKQNSKLVSTNTVTAH-IKPTFFVCMALSL 336
Db VVSTAIQALN-----KAIIPYFVALRKQKLV-----VQQLHKWALFSFLIP 294
QY 337 TLCFVFWFTPNVSEKILIDIGVDPAFALCVLRLRIFSPFPVTVRAHLTGLMTLKK 396
Db LIMWI-----IPEDVLVWILGQVGVGYFIFLSTLSIYLI-----LVNLYFYGK 345
QY 397 TFLVAPSSVLRIRIIVLISLVL-----PYLGVHGA 426
Db NKLIQCSVLSTIIIVASLVALTFTETIKYIPVAGIIGS 383

RESULT 15

HPPI_METAC STANDARD; PRT; 676 AA.
AC Q8TJA9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate-energized proton pump 1 (EC 3.6.1.1) (Pyrophosphate-
energized inorganic pyrophosphatase 1) (H+-Ppase 1) (Membrane-bound
proton-translocating pyrophosphatase 1).
GN HPPA1 OR MA3879.
OC Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Zimmo L., Maylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Zimmo L., Barber R.D., Cann I., Graham D.E., Grahame D.A., Ye W., A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Perry J.G., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Pritchett M., Sowers K.R., Jing H., Macario A.J.L., Paulsen I.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity.";
RL Genome Res. 12:532-542(2002).
CC -|- FUNCTION: Generates a proton motive force; it probably catalyzes a
fully reversible reaction, thus being able to synthesize
pyrophosphate when the proton motive force is sufficient (By
similarity)
CC -|- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -|- COFACTOR: Magnesium and potassium (By similarity).
CC -|- SUBUNIT: Homodimer (potential).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -|- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
(TC 3.A.10) family. Subfamily 1.
CC
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CC
CC EMBL; A011099; AAM07230.1; ALT_INIT.
DR HAMAP; MF_01129; -; 1.
DR InterPro; IPR004131; H_Ppase.
DR Pfam; PF03030; H_Ppase; 1.
DR TIGRfams; TIGR01104; V_Ppase; 1.
KW Hydrogen ion transport; Hydrolase; Magnesium; Potassium;
KW Transmembrane; Complete proteome.

FT	TRANSMEM	4	23	Potential.
FT	TRANSMEM	57	79	Potential.
FT	TRANSMEM	84	106	Potential.
FT	TRANSMEM	127	149	Potential.
FT	TRANSMEM	153	181	Potential.
FT	TRANSMEM	237	259	Potential.
FT	TRANSMEM	264	286	Potential.
FT	TRANSMEM	299	321	Potential.
FT	TRANSMEM	326	348	Potential.
FT	TRANSMEM	389	411	Potential.
FT	TRANSMEM	472	494	Potential.
FT	TRANSMEM	501	523	Potential.
FT	TRANSMEM	568	587	Potential.
FT	TRANSMEM	594	616	Potential.
FT	TRANSMEM	653	675	Potential.
FT	SITE	463	463	DETERMINANT OF POTASSIUM DEPENDENCE (BY SIMILARITY).
SQ	SEQUENCE	676 AA; 69276 MW; 5C7144B63F1F8E26 CRC64;		
Query Match				
Best Local Similarity 4.2%; Score 105; DB 1; Length 676;				
Matches 88; Conservative 50; Mismatches 145; Indels 136; Gaps 17;				
Qy	72	VGLVFNKSDRTKAVLCMVVAGIAVHFTLIAYSIDLGYIINKLHVHVESVGSKTTRA	131	
Db	281	VGTFVTRTKTESAIHMAFNGLIAAILTVIA---SYFVTS-----	320	
Qy	132	FLYLAAPPFMDAMANTHAGILLKHYSFLVGCASISDVIAQVVFVAILLHSHLECREPLL	191	
Db	321	-----MLLGEYGLNVFFATVAGLVAGFLIGQITEHYTSYDKKPTL	360	
Qy	192	IPILSLWYGALVRCTTLCIGVYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALILATQ	251	
Db	361	RVANSCQTGS---ATNIITGFAK-----GMESTL-----WPVVIISIAL	396	
Qy	252	RISRPVNLVFSRDLGSSAATEAVAILTATY-PVGHMPYG-----WLTEIRAVYPAPD	304	
Db	397	YIAPQLSGLYGIATAAVGMLATLIGISLSDVAYGPVADNAGGIAEMSHQKEEVQRITD	456	
Qy	305	KNPSPKLVSTSNVTAAHIKKTFFVCMALSLTLCFWMF-----WTENVSEKIL	353	
Db	457	-----AVGNT-TAAIGKGFAGSAAJTALAFASYGIANGLSAIDVMNENFVIGLT	506	
Qy	354	I-----DIIGVDFAFaelcVVPLRIFSPFPVTVRAHLTGWMLTK-----K	396	
Db	507	IGAMLPYLFSSMTILAVGNAAGEVVVEVRQF-----REIAG-LMEGRADPDYK	555	
Qy	397	TFVLAPGSVLR-----IIVLIASLVLPYLGVHGATLG---VGSLLAGFVGESTWAI	446	
Db	556	CIAISTHSALKEMIPPGLLAVIAFLV-----GLVLGPGALGGLLAGSVASGFMIAT	607	

Search completed: April 22, 2004, 13:56:56
Job time : 21 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 13:43:23 ; Search time 7332 Seconds
(without alignments)
11994.561 Million cell updates/sec

Title: US-09-978-188A-6

Perfect score: 2945

Sequence: 1 cgcctgcgcgcgcgcgcctc.....aatgctctatacaaaaaa 2945

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_nam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1575.2	53.5	2980	11	BC042644
2	1566.2	53.2	3497	11	AK083135
3	1264	42.9	1383	29	AY417273
4	1049.6	35.6	1383	29	AY417275

5	998	33.9	1047	29	AY417274
6	932.6	31.7	1059	13	BX385283
7	884.6	30.0	961	13	BX349262
8	748.4	25.4	1913	11	AK086014
9	737	25.0	771	14	CA447218
10	735.2	25.0	760	10	BE793798
11	720.4	24.5	737	13	BU615215
12	718.8	24.4	723	10	BE876197
13	717.4	24.4	732	12	BQ014252
14	717	24.3	729	12	BQ009716
15	715	24.3	726	14	CB241863
16	713.4	24.2	747	13	BX094550
17	709	24.1	719	13	BQ182147
18	709	24.1	719	13	BQ182504
19	693.2	23.5	995	12	BM547717
20	689	23.4	1099	12	BQ054819
21	676.8	23.0	737	9	AU133975
22	676.4	23.0	702	12	BG567677
23	660.2	22.4	675	10	AW170131
24	658.8	22.4	677	14	CA424729
25	658.4	22.4	660	14	CA391971
26	657	22.3	744	13	BQ446398
27	650.4	22.1	662	13	BU619797
28	649.8	22.1	674	14	CD591535
29	633.6	21.5	706	9	AV723948
30	626.4	21.3	951	12	BG178057
31	616	20.9	634	13	BU078281
32	614.2	20.9	636	14	CK301088
33	614.2	20.9	729	10	AW836234
34	611	20.7	881	13	BU125674
35	604.4	20.5	657	14	CA446160
36	602	20.4	729	12	BG104819
37	598.8	20.3	902	13	BQ900763
38	598.6	20.3	664	12	BG714293
39	593.2	20.1	617	10	AW608052
40	590	20.0	641	13	BQ184793
41	589.6	20.0	1191	12	BM546571
42	588.8	20.0	592	13	BU078033
43	588.6	20.0	817	10	BE744331
44	585.6	19.9	711	13	BY741290
45	583.2	19.8	638	13	BQ640543

ALIGNMENTS

RESULT 1	BC042644	2980 bp	mrna	linear	HTC 17-DEC-2003
LOCUS	BC042644	Mus musculus cDNA clone IMAGE:3499832, containing frame-shift errors.			
DEFINITION	BC042644	Mus musculus (house mouse)			
ACCESSION	BC042644	GI:27503560			
VERSION	BC042644.1				
KEYWORDS	HTC				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	1 (bases 1 to 2980) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, A.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Hale, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,				

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2980)
 Strausberg, R.
 Direct Submission
 Submitted (02-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.ncbi.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 61 Row: C Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994166
 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
 1..2980
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:349832"
 /tissue_type="Mammary tumor, C3(1)-tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
 /clone_lib="NCI COAP Mam6"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 53.5%; Score 1575.2; DB 11; Length 2980;
 Best Local Similarity 77.7%; Pred. No. 0;
 Matches 2297; Conservative 0; Mismatches 488; Indels 191; Gaps 25;
 QY 13 CGCCCCCTCCCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTGGGGTTCAGCCAC 72
 Db 183 CTCGCGCGCTCCCGCAGCAGTGCCTCGCGGAGCAGATGTGTGGGGTTCAGCCAC 242
 QY 73 GCGGGGACTATGTGAATTCGCGGCTCAGCAGTGTGTGGGGTTCAGCCAC 132
 Db 243 GCGGGGACTATGTGAATTCGCGGCTCAGCAGTGTGTGGGGTTCAGCCAC 302
 QY 133 GGTGCCCCCTGGGCATCACCACATAGCATCGACTTCGGGAGCAGCCCTGAACCGGG 192
 Db 303 GGTGCCCCCTGGGCATCACCACATAGCATCGACTTCGGGAGCAGCCCTGAACCGGG 362
 QY 193 CATTGCTGCTCAAGGAGATGTAGTGTGAGATGCTGCGCAGCTACGGGCTGGGTTCTC 252
 Db 363 CATGCTGCTCAAGGAGATGTAGTGTGAGATGCTGCGCAGCTACGGGCTGGGTTCTC 422
 QY 253 CCTCATGAAGTCTTCACGGGTCCCATGAGTGTCTCAAAATGTGGGCTGGGTTGT 312
 Db 423 TTGATGAGTCTTCACGGGGCCCATGAGTGTCTCAAAATGTGGGCTGGGTTGT 482

QY 313 GAACAGCAAGAGAGACAGGACCAAGCGCTCTCTGTATGTGTGGAGGGGCGATCGC 372
 Db 483 GAACAGCAAGAGAGACAGGCGCAAGCGCTCTCTGTATGTGTGGAGGGGCGATCGC 542
 QY 373 TGCCTGCTTTCACACACATGATAGCTTATAGTATTAGGATACATATCAATAAACT 432
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 QY 433 GCACCATGTGACGAGTCGCTGGGGAGCAAGAGAGGGGCTTCTGTACTCTGCGGC 492
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 QY 493 CTTTCTCTTTCAGGACGCAATGGCATGACCCATGCTGGCATTTCTTTAAACACAAATA 552
 Db 663 CTTTCTCTTTCAGGATGCCATGGCGTGCATCTGCTGGCATTTCTTTAAACACAAATA 722
 QY 553 CAGTTTCTGTGGAGTGCCTCAATCTCAGATGTATAGCTCAGGTGTGTTTGTAGC 612
 Db 723 CAGTTTCTGTGGAGTGCCTCAATCTCAGATGTATAGCTCAGGTGTGTTTGTAGC 782
 QY 613 CATTGTTGCTTTCACAGTCACTGCGGAGCGGCGCTGCTCATCCGATCCCTCTCT 672
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 QY 673 GTACATGGGCGCATTTGTGCGCTGCACCACTGTGCTGTGGCTACTCAAGAAACATCA 732
 Db 843 GTACATGGGCGCATTTGTGCGCTGCACCACTGTGCTGTGGCTACTCAAGAAACATCA 902
 QY 733 CGACATCATCTCTGACAGAGTGGCGGAGTGCAGTGGGAGATGCAACAATAGAAAGAT 792
 Db 903 CGACATCATCTCTGACAGAGTGGCGGAGTGCAGTGGGAGTGCAGTGGGAGATGCAACAATAGAAAGAT 962
 QY 793 GCTGAGCTTCTGTGGCTTGTGGCTCTAATTTCTGCCCAACAGAGAAATCAGTTCGGCT 852
 Db 963 GCTGAGCTTCTGTGGCTTGTGGCTCTAATTTCTGCCCAACAGAGAAATCAGTTCGGCT 1022
 QY 853 TGTCAACCTCTTGTGCTGGGAGCTTGTGGAGTCTGTGAGCCACAGAGGAGTGGC 912
 Db 1023 TGTCAACCTCTTGTGCTGGGAGCTTGTGGAGTCTGTGAGCCACAGAGGAGTGGC 1082
 QY 913 GATTTTGACAGCCACATACCTGTGGGTCAATGATGATGATGATGATGATGATGAT 972
 Db 1083 CATTCTGACAGCCACATACCTGTGGGTCAATGATGATGATGATGATGATGATGAT 1142
 QY 973 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1032
 Db 1143 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
 QY 1033 CACAGTCAAGGAGCCACATCAAGAGTTCACCTGCTGTGATGCTGTGATGATGAT 1092
 Db 1203 CACAGTCAAGGAGCCACATCAAGAGTTCACCTGCTGTGATGCTGTGATGATGAT 1261
 QY 1093 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
 Db 1262 -CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
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 Db 1441 CTTGCTCTTTCGCGGAGTGTGCTGGGAGTCTGCTGCTCATCGGAGCTGGTGGT 1500
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 Db 1501 CTTGCTCTTTCGCGGAGTGTGCTGGGAGTGTGCTGGGAGTGTGCTGGGAGTGT 1560

QY	973	TGCTGTGTATCCTCTGCTTTTCGACAAGAATAAACCCACGACAAACAACTGGTGAGCACGAGCAA	1032
Db	1219	GGCTGTCTACCTCTGCTTTTGACAAGAATAAACCCACGACAACTGGTGAGCACGAGCAA	1278
QY	1033	CACAGTCACGGCAGCCACACATCAAGAGAGTTCACTTCGTCTGCATGGCTCTGTCACTCAC	1092
Db	1279	CACGGTCACCTCAGCCACACATCAAGAGAGTTCACTTCGTCTGCATGGCGCTGTGGCTGAC	1338
QY	1093	GCTCTGTTTCGTGATGTTTTTGGACACCCACAGTGTCTGAGAAAAATCTTGATAGACATCAT	1152
Db	1339	GCTCTGTTTGTGATGTTCTGGACCCCAACGCTCTGAGAGATTCTGATAGATATCAT	1398
QY	1153	CGAGTGGACTTTGGCTTTTCGAGAACTCTGTGTGTTTCCTTTGCGGATCTTCTCCTTCCT	1212
Db	1399	TGAGTGGACTTTGGCTTTTCGAGAACTCTGTGTGATCTCTCTCGGTATCTTCTCTCTCT	1458
QY	1213	CCCAGTTCACAGTCACAGTGAAGGCGCATCTCACCGGCTGGCTGATGACACTGAAGAAAAAC	1272
Db	1459	CCCAGTGCCAGTGACTGTGAGAGCTCATCTCACTGGATGGCTGATGACACTGAAGAAAAAC	1518
QY	1273	CTTTCGTCTTTGCCCGCAGCTCTGTCTGGGATCATGCTCCTCATCGCAGGCTCTGGGT	1332
Db	1519	CTTTGTGCTGGCGCCAGCTCGGTCTGGCCATCATGCTCCTCATCACCAGCCTTTGGGT	1578
QY	1333	CCTACCTACTCTGGGGTGACAGGTGCGACCCCTGGGCGTGGGCTCCCTCTCGCGGGCTT	1392
Db	1579	CCTGCCGTACTCTGGGGTGACAGGAGCCACACTAGGTGTGGGCTCCCTCTAGCAGGTT	1638
QY	1393	TGTGGGAGATCCACATGCTCGCCATCGCTGGTGCTATGTTCTACGGNAGCAGAAAAA	1452
Db	1639	TGTGGGAGATCTACCATGTTGCCCTTGCAGCATGCTATGTTCTACGAAAAACAGAAAA	1698
QY	1453	GAAGATCGAGAAAGAGTCGGCCACGGAGGGGGAAGACTCTGCCATGACACATGCTCTC	1512
Db	1699	GAAGATCGAGAAAGAGTCAGCTCAGCCACGGAGGGAGAGACTCGGCCATGACGACATGCTCTC	1758
QY	1513	GACAGAGAGGTGACAGACATCTGTGGAATGAGAGAGGAGAGATGAATAAG-CACAGGGAC	1571
Db	1759	AACAGAGAGGTTCACACATCTGTAGATGAGAGAGAGAAATAGTAAGACAGAGCTGC	1818
QY	1572	GCCATGGGCACTGCAGGAGCGGTCAAGTCAGAGTGCACATTCGGCATCATCTCTTCCTCTCT	1631
Db	1819	TGGGGGCCACCGCAGGACAGTCAG-GACAAACAATGTCGTCTCTTCCTCTCTCTCT	1877
QY	1632	CCCATCGTATTTTGTTCCTTTTTTTTGTGTTT-TTGTATATGAAGAGGCTTGATT	1690
Db	1878	CCCATCAAGTTGTTTCTGTGTTTAAATTTTATTTCTGTGTTATGAAGAGGCTTGATT	1937
QY	1691	TAAAGGTTTCGTGTCATTTCTAGCATACTGGGTATGCTCACACTGACGGGGGACCTTA	1750
Db	1938	TAGAGGTTTCGTATAAATCTTAGCATACTGGGTATGCT-CACCGATCAGGGACCTG	1995
QY	1751	GTGAATGGTCTTTACTGTGTTATGTAAAAACAACGAAACAACACTGACTCATCCCTG	1810
Db	1996	AAGAAAGGCTTTTACTCTGCTTTGTA-----ACTCAGAAATCGGTGACTTTCACGCCCCG	2050
QY	1811	CCTCAGAAAAACCAAAAGACACAGCTGCCTCAGGTTGAGTTGTCCTCTCTCCCTG	1870
Db	2051	CTTCA-THAAACCAAAAGATAGAGCTTGCTCTTGGTCAAGTTT---CTACTCCCTG	2105
QY	1871	GACAATCTCTTC-TTGGAAACAAAGGACTGACGTGTGGCCATCGCGCTCGGTCACCCTG	1929
Db	2106	GACAATCTCCAATTGGAAACCAAGGACTTG-----	2136
QY	1930	CACAGCAGGCCACAGACTCTCTCTGCCCTTTCGCTCTTAAGAATCAACAGGTTAAA	1989
Db	2137	-----GGCCAGACTTTTCTGTTTCAATGTTTGGCTCTCTTAGATATCAACAGGTTGAA	2189
QY	1980	ACTCGGCTTCCTTGAATTTGTTCCCACTGACATGGCGGTACAAAGAGATGGAGCCCCGG	2049
Db	2190	GCTCAGCCTCTCTTGACTTGTGCTCCCAACACTGTGGCTCT-----	2229

QY	2050	TGGCCTCTTAAATTTCCCTTCTCGCAGGAGTTCGAAA	CCATCTACTTCCACACATCGAGG	2100
DB	2230	-----GGAGTCATGAACATATCTGCGGCACATA	-----C	2257
QY	2110	AGCGGGTGGCAGCTCAGCCCGAGTCCCCCGTT	CACACTGAGGAACGAGGACCTGTGA	2169
DB	2258	TGGTGGCCCCAGGCTGACAGCCACAGTCCCTGTT	CCCGAGGAAGGCGTGGTGGCCCC	2317
QY	2170	CCACAGCAGGCTGACAGATGGACAGAAATCTCC	CGTAGAAAGGTTTGGTTTGAATGCCCC	2229
DB	2318	TGCTGGGCCCAACGTAGTGGGAATTTTATCTCC	TGTAGAAATGGGTCAAGTCA	2369
QY	2230	GGGGGACGAACTGACATGGTTGAATGATAGACAT	TTCACCTCTCGGTTCTCCCTAGATCTG	2289
DB	2370	-----CCAACTGACTTGATCGTCAGCATCCCAT	TGTTTCTCGTTTCACTGAGTTG	2421
QY	2290	AGCAAGCTGTCAAGTTCTCACCCCCACCGTGTA	TATATACATGAGCTAACTTTTTTAAATTGT	2349
DB	2422	-----CCGCACCCACAGTGTATATACATGAGCT	GACTTTTTTCAGAGGCTGT	2466
QY	2350	CACAAAGCGCATCTCCAGATTCAGACCCCTCG	CGCATGACTTTTCTCGAAGCGCTTGCCT	2409
DB	2467	CCCGAAGTGCAGCTCCAGTGTGACACCTT	-CGCATGAGTTTCCCTGGAAGGCTTGCCT	2525
QY	2410	TTCCCTCGCCTTTCCTGAAGGTGCGATTAGAG	CGAGTCACATGAGCAATCCTAACTTTGC	2469
DB	2526	TT-ACTCGCCTTCCCTGAAGATGCACTAGAGG	AG--AAGTGGAGCGTTCTAACTGTCC	2582
QY	2470	AT-----TTTAGTTTTTACAGTGAACCTGA	AGCTTTAAGTCTCATCCAGCA	2514
DB	2583	ATTTCCTAACTGTGCCATTTTCGTTTTTCA	CAGTGAAGCTTTAAGTCTGAATCTAGCA	2642
QY	2515	TTCTAATGCCAGGTGCTGTAGGTAACCTTT	TGAAGTGTAGATATATTAACCTGGTTCTGCTA	2574
DB	2643	TCCTAATGSCAGGCTCTGTCTCGTAACCT	TCTGATGTAGATGTGCCGCCTATTTT	2696
QY	2575	TCCTTAGTCATAACTCTCGCGGTACAGTAAT	TGGAATGTACTACGGTACTCCCTCCCA	2634
DB	2697	-----CTGCGGACAGGTAAACCGAG--TG	TACTATGGTACTCCCTT	2735
QY	2635	CACCATACGATAAAGCAAGACATTTTAT	-AACGATACCAGAGTCACATATGTGTCCTCCC	2693
DB	2736	--CCACACCATTAAGCAAGACATTTTATA	AACAGTATCAAGGTCACATGTGTATAC-CCC	2792
QY	2694	TGAATAACGGATTCGAAATCCATGCGAGTGC	AGTATATTTTCTAAAGTTTTGGAAAGCAG	2753
DB	2793	GGAAATATGCAATTGGAAATCCACTAGTCAG	TATATTTTCTAAAGTTTTTGGAAAGCGG	2852
QY	2754	GTTTTTTCCCTTT-AAAAAATTAAGACACG	GTTCACCTAAAT--TCATTTAGTCAGAAT	2809
DB	2853	GTTTTTTCTTTAAAAAATTAAGACACAG	TTCACTAAATTCCTGATTTAGTCAAAAGT	2912
QY	2810	TCCTAGACTGAAGAACCTAAACAAA-AAA	TATTTTAAAGATATAAATATATGCTGTAT	2868
DB	2913	AACTAGACTGAAGAACCTAAACAAAATA	TATTTTAAAGATATAAATATATGCTGTAT	2972
QY	2869	ATGTTATGCTAATTTATTTTAGGCTATAAT	CATTTCTCTATTTTCGCATTTTCAATAAAAT	2928
DB	2973	ATGTTATGCTAATTTATTTTAGGCTATAAT	CATTTCTCTATTTTCGCATTTTCAATAAAAT	3032
QY	2929	GTCTCTAATACAA	2941	
DB	3033	GTCTCTAATACAA	3045	

RESULT 3	
AV417273	1383 bp DNA linear GSS 17-DEC-2003
LOCUS	Homo sapiens ANKH gene, partial sequence,
DEFINITION	VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION	genomic survey sequence.
VERSION	AV417273
KEYWORDS	AV417273.1 GI:39773233
	GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1383)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1383)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1383
/gene="ANKH"
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ORIGIN
Query Match 42.9%; Score 1264; DB 29; Length 1383;
Best Local Similarity 91.4%; Pred. No. 6.2e-254;
Matches 1264; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 179 GCCTTGAACCGGGGATTCGCTGCTCAAGAGAGATGCGATCGAGATGCTGGCAGCTAC 238
Db 1 GCCTTGAACCGGGGATTCGCTGCTCAAGAGAGATGCGATCGAGATGCTGGCAGCTAC 60
QY 239 GGGCTGGGGTACTCCCTCATGAAGTTCCTACGGGTCCCATGAGTGACTTCAAAAATGTG 298
Db 61 GGGCTGGGGTACTCCCTCATGAAGTTCCTACGGGTCCCATGAGTGACTTCAAAAATGTG 120
QY 299 GGCCTGGTGTGTGAAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTG 358
Db 121 GGCCTGGTGTGTGAAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTG 180
QY 359 GCAGGGCCATCGCTCCGCTCTTTCACACACTGATAGCTTATAGTATTTAGGATAC 418
Db 181 GCAGGGCCATCGCTCCGCTCTTTCACACACTGATAGTATTTAGGATAC 240
QY 419 ATTATCAATAACTGCACCATGTGGACAGTGGTGGGAGCAAGACGAGAGGGCCTTC 478
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QY 479 CTGTACCTCGCGCCTTTCCTTTCATGACGCAATGGCATGGACCATGCTGGCATTC 538
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Db 361 TTAAACACAAATACAGTTTCCTGGTGGGATGTGCTCAATCTCAGATGTATAGCTCAG 420
QY 599 GTTGTGTTGTAGCATTTTGTGTTACAGTACCTGGAATCGCGGAGCCCTGCTCATC 658
Db 421 GTTGTGTTGTAGCATTTTGTGTTACAGTACCTGGAATCGCGGAGCCCTGCTCATC 480
QY 659 CCGATCCTCTCCTGTATACATGGGCGCATTTGTGCGCTGCACACCCCTGTGCTGGGCTAC 718
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719 TACAAGAACATTTCACGACATCATCCCTGACAGAGAGTGGCCCGGAGCTGGGGGAGATGCA 778
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779 ACAATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAAATCTGGCCACACAGAGA 838
601 ACAATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAAATCTGGCCACACAGAGA 660
839 ATCAGTGGCCCTATTTGTCAACCTCTTTGTTCCCGGACCTTGGTGGAGTCTTCGAGCC 898
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899 ACAGAGGACAGTGGCGATTTTGACAGCACATACCTGTGGGTGCATGCTACACGCTGG 958
721 ACAGAGGACAGTGGCGATTTTGACAGCACATACCTGTGGGTGCATGCTACACGCTGG 780
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781 TTGACGGAATCCGCTGCTGTGATCTGCTGTCGACAAAGATAAACCCAGCAACAAACTG 840
1019 GTGAGCAGCAGCAACACAGTGCAGCGCAGCCACATCAAGAGTTTCCCTGCTGTCATG 1078
841 GTGAGCAGCAGCAACACAGTGCAGCGCAGCCACATCAAGAGTTTCCCTGCTGTCATG 900
1079 GCTCTGTCTACTCAGCTCTGTTTCGTGATGTTTGGACACCCCAACGCTGTGAGAAATC 1138
901 GCTCTGTCTACTCAGCTCTGTTTCGTGATGTTTGGACACCCCAACGCTGTGAGAAATC 960
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961 TTGATAGACATCATCGGAGTGGACTTGCCTTTGAGAACTCTGTGTTTCCCTTTCGG 1020
1199 ATCTTCTCTCTTCCAGTTCACAGTGCAGGAGCGCATCTCACCGGCTGGCTGATG 1258
1021 ATCTTCTCTCTTCCAGTTCACAGTGCAGGAGCGCATCTCACCGGCTGGCTGATG 1080
1259 ACATGAAAGAAACCTTGGTCTGCTCCCGCAGCTCTGTGCTGGATCATGCTCTCATC 1318
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1201 CTCCTGGCGGCTTGTGGGAGAAATCCACCATGTCGCATCGCTGCTGCTATGCTAC 1260
1439 CGAAGCAGAAAAGAGATGAGATGAGTGCAGCGTGCAGCGTGGACCCCTGGGAGAGACTCTGCCATG 1498
1261 CGAAGCAGAAAAGAGATGAGATGAGTGCAGCGTGCAGCGTGGAGAGACTCTGCCATG 1320
1499 ACAGACATGCTCCGACAGAGAGTGCAGACATCTGCGAAATGAGAGAGAGAGTAA 1558
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1559 TAA 1561
1381 TAA 1383

RESULT 4
AY417275
LOCUS 1383 bp DNA linear GSS 17-DBC-2003
DEFINITION Mus musculus ANKH gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY417275
VERSION AY417275.1 GI:39773235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 1383)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1383)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>1383
/genes="ANKH"
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ORIGIN
Query Match 35.6%; Score 1049.6; DB 29; Length 1383;
Best Local Similarity 81.7%; Pred. No. 4.8e-209;
Matches 1130; Conservative 0; Mismatches 253; Indels 0; Gaps 0;
QY 179 GCCTTGAACCGGGGCATTGCTGCTGCAAGGAGGATGCGAGATGCTGCCAGCTAC 238
DB 1 GCCTTGAACCGGGGCATCGCTGAGTCAAGGAGGATGCGAGATGCTGCCAGCTAC 60
QY 239 GGCTCGGCTACTCCCTCATGAAGTTCTTCAAGGTCCTCATGAGTACATCAAAATGTG 298
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DB 121 GGCTCGGCTACTCCCTCATGAAGTTCTTCAAGGTCCTCATGAGTACATCAAAATGTG 180
QY 359 GCAGGGGCCATCGCTCGGCTCTTCAACACATGATAGCTTATAGTGATTAGGATACTAC 418
DB 181 GCCGGTGCCATCGCTCGGCTCTTCAACACATGATAGCTTATAGTGATTAGGATACTAC 240
QY 419 ATTATCAATAAATGACCATGTCGACGAGTCGGTGGGAGCAAGACGAGAGGCGCTTC 478
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DB 421 GTTGTGTTTCTAGCCATTTTGTCTTCAAGTCACTGGAATGCGGAGCCCTGCTCATC 480
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DB 481 CCCATCCTCTCTGTACATGGGTCGCTGTGCTGCTGCACACCTGTGCTGGGCTAC 540
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DB 541 TACAGAACATTCACGACATCATCCCGACAGAGCGGCCCATGAGCTGGGGGATGCA 600

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QY 1559 TAA 1561
DB 1381 TAA 1383
RESULT 5
AY417274 1047 bp DNA linear GSS 17-DEC-2003
LOCUS Pan troglodytes ANKH gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY417274
VERSION AY417274.1 GI:39773234
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 1047)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
 Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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ORIGIN
 Query Match 33.9%; Score 998; DB 29; Length 1047;
 Best Local Similarity 95.6%; Pred. No. 3.1e-198;
 Matches 1001; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 515 GCATGGACCCATGCTGGGATCTCTTAAACACAAATACAGTTTCCTGGTGGGATGGCC 574
 Db 1 GCATGGACCCATGCTGGGATCTCTTAAACACAAATACAGTTTCCTGGTGGGATGGCC 60
 QY 575 TCAATCTCAGATGTCATAGTCAGGTGTTTTGTAGCAATTTGCTTCACAGTCACCTG 634
 Db 61 TCAATCTCAGATGTCATAGTCAGGTGTTTTGTAGCAATTTGCTTCACAGTCACCTG 120
 QY 635 GAATGCGGGAGCCCTGCTATCCGATCTCTCTTGTACATGGGGGCACTGTGGCC 694
 Db 121 GAANNCCGGAGCCCTNNNNNTCCGATCCNNNNCTTGTACATGGGNNNNCTTGTGGC 180
 QY 695 TGCACACCCCTGCTGGCTGGCTACTACAGAACTTCACGATCATCCCTGACAGAGT 754
 Db 181 TGNNNNNCTGTGCTGNNNNNACAGAACTTCACGATCATCCCTGACAGAGT 240
 QY 755 GGCCTGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGTGGCCTTG 814
 Db 241 GGCCTGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGTGGCCTTG 300
 QY 815 GCTCTAATCTGCGCACACAGAGATCAGTCGGCTATTGTCAACTCTTTGTTCCGG 874
 Db 301 GCTCTAATCTGCGCACACAGAGATCAGTCGGCTATTGTCAACTCTTTGTTCCGG 360
 QY 875 GACCTTGTGGGAGTTCTGCAGCCACAGAGGAGTGGGATTTTGACAGCCACATACCT 934
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 QY 935 GTGGGTACATGCCATACCGCTGTTGACGGAAATCCGCTGTGTATCTCTGCTTCGAC 994
 Db 421 GTGGGTACATGCCATACCGCTGTTGACGGAAATCCGCTGTGTATCTCTGCTTCGAC 480
 QY 995 AAGAATAACCCAGCAACAACTGTGAGCAGCAGCAACACAGTCACGGCAGCCACATC 1054
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 QY 1055 AAGAATTACCTTCCTGTGATGGCTCTGTCACTCACGCTCTGTTGTGATGTTTGG 1114
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 QY 1115 ACACCAACCTGCTCAGAAATCTTGTATAGATCATCGGAGTGGACTTCCCTTGA 1174
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 Db 901 GCCATCGTCTGCTGATGTTCTACCGAGACAGAAAAGAGATGAGAAATGAGTCGGCC 960
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RESULT 6
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 DEFINITION Homo sapiens cDNA clone CS0DL009YC05 5-PRIME, mRNA sequence.
 ACCSSION BX385283
 VERSION BX385283.1 GI:30447347
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1059)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3147.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DL009AB03QPI&cluster=3147.r. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0DL009AB03QPI.

FEATURES
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

[illegible]

BX349262 961 bp mRNA linear EST 05-MAY-2003
 BX349262 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 Homo sapiens cDNA clone CS0DL009YC05 5-PRIME, mRNA sequence.
 BX349262
 BX349262.1 GI:30371351
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 961)
 Li W.B., Gruber C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sagref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3147.r.For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BAG057ZA10_CS05449_1&cluster=3147.r.
 Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0BAG057ZA10_CS05449_1.
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 30.0%; Score 884.6; DB 13; Length 961;
 1 Similarity 95.9%; Pred. No. 1.7e-174;
 915; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
 9 GAGGCTTCATTAAAGTTTCGTGTCAAATTCCTAGCATACTGGGTATGCTCACACTGA 1738
 1 GAGGCTTCATTAAAGTTTCGTGTCAAATTCCTAGCATACTGGGTATGCTCACACTGA 60
 39 CGGGGGGACCTAGTGAATGGTCTTTACTGTGCTATGTATATAAAACAAACGAAACAACTGAC 1798
 61 CGGGGGGACCTAGTGAATGGTCTTTACTGTGCTATGTATATAAAACAAACGAAACAACTGAC 120
 99 TTCATACCCCTGCCTCAGAAAACCCAAAGACACAGCTGCCTCAGCGTTGACGTTGTGT 1858
 121 TTCATACCCCTGCCTCAGAAAACCCAAAGACACAGCTGCCTCAGCGTTGACGTTGTGT 180
 59 CTTCTCCCTCGACAAATCTCTCTTGGAAACCAAGAGCTGACGCTGTGCCATCGCGCCT 1918
 81 CTTCTCCCTCGACAAATCTCTCTTGGAAACCAAGAGCTGACGCTGTGCCATCGCGCCT 240
 119 CGGTACCTTCACAGCAGGCCACAGACTCTCTGTCCCTTCATCGCTCTTAAGATC 1978
 141 CGGTACCTTCACAGCAGGCCACAGACTCTCTGTCCCTTCATCGCTCTTAAGATC 300
 79 AACAGGTTAAACTCGGCTTCCTTTTCATTTCCTTCCAGTTCATATGGCCGCTACAAAGAGA 2038
 01 AACAGGTTAAACTCGGCTTCCTTTGATTTGCTTCCAGTTCATCGCTCTTAAGATC 360
 9 TGGAGCCCGCGTGGCTCTTAAATTTCCCTTTGCCACGGAGTTGGAACCAATCTACTCC 2098

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 95-123, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
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/note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP E10 is a cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACCTGGAC.
TAG TISSUE=chondrosarcoma
TAG_LIB=UI-H-E10
TAG_SEQ=ACACCTGGAC"

ORIGIN
Query Match 25.0%; Score 737; DB 14; Length 771;
Best Local Similarity 99.7%; Pred. No. 1.4e-143;
Matches 748; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2196 ATCTCCCGTAGAAGGTTGGTTTGAATGCCCGGGGCGACCACTGACATGGTTGAA 2255
DB 759 ATCTCCCGTAGAAGGTTT-GTNTGAATGCCCGGGGCGACCACTGACATGGTTGAA 701
QY 2256 TGATAGCATTTTCACCTCGGTCTCTAGATCTGAGCAAGCTGTGAGTCTCACCCCCAC 2315
DB 700 TGATAGCATTTTCACCTCGGTCTCTAGATCTGAGCAAGCTGTGAGTCTCACCCCCAC 641
QY 2316 CGTGATATACATGAGCTAACTTTTAAATTTGTCACAAAGCGCATCTCCAGATTCGAG 2375
DB 640 CGTGATATACATGAGCTAACTTTTAAATTTGTCACAAAGCGCATCTCCAGATTCGAG 581
QY 2376 ACCCTGCCGATGACTTTTCCGAGGCTTGCTTTTCCCTGCCCTTCTCGAAGTGCA 2435
DB 580 ACCCTGCCGATGACTTTTCCGAGGCTTGCTTTTCCCTGCCCTTCTCGAAGTGCA 521
QY 2436 TTAGAGCGAGTCACATGGAGCATCTTAATTTGCAATTTAGTTTTCAGTGAACGTGAAG 2495
DB 520 TTAGAGCGAGTCACATGGAGCATCTTAATTTGCAATTTAGTTTTCAGTGAACGTGAAG 461
QY 2496 CTTTAAGTCTCATCCAGATTTCTATCCAGGCTGCTGTAGGTAACCTTTTGAAGTAGAT 2555
DB 460 CTTTAAGTCTCATCCAGATTTCTATCCAGGCTGCTGTAGGTAACCTTTTGAAGTAGAT 401
QY 2556 ATATTACCTGGTTCTCTATCTCTAGTCATAACTCTGGGTACAGGTAATTGAGATGTA 2615
DB 400 ATATTACCTGGTTCTCTATCTCTAGTCATAACTCTGGGTACAGGTAATTGAGATGTA 341
QY 2616 CTACGGTACTTCCCTCCACACATACGTAAGGACATTTTATACGATACACGAG 2675

Db 340 CTACGGTACTTCCCTCCACACATACGTAAGGACATTTTATACGATACACGAG 281
QY 2676 TCACATATGTGTCCTCCCTGAAATTAACCATTCGAAATCCATGCGTGCAGTATATTTT 2735
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QY 2796 GATTTAGTCAGAAATTCCTAGACTGAAAGACCTAAACAAAAAATTTTAAAGATATAA 2855
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QY 2856 ATATATGCTGTATATGTTATGTAATTTATTTAGGCTATATACATTTTCCATTTTCGCA 2915
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RESULT 10
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DEFINITION mRNA sequence.
ACCESSION BE793798
VERSION BE793798.1 GI:10214996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 760)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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High quality sequence stop: 719.
Location/Qualifiers
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ORIGIN
Query Match 25.0%; Score 735.2; DB 10; Length 760;
Best Local Similarity 98.8%; Pred. No. 3.4e-143;
Matches 751; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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185	Qy	AACCGGGCATTTGCTGCTCAAGAGGATGCACTCGAGATGCTGGCAGCTACGGGCTG	244
61	Db	AACCGGGCATTTGCTGCTCAAGAGGATGCACTCGAGATGCTGGCAGCTACGGGCTG	120
245	Qy	GGGTACTGCTCATGAAGTTCTTACGGGTCCCATGATGACTTCAAAAATGTGGCCCTG	304
121	Db	GGGTACTGCTCATGAAGTTCTTACGGGTCCCATGATGACTTCAAAAATGTGGCCCTG	180
305	Qy	GTGTTTGTGAACAGCACAAGAGACAGGACCAAGACCGTCTGTGTATGTTGGTGGCGAGG	364
181	Db	GTGTTTGTGAACAGCACAAGAGACAGGACCAAGACCGTCTGTGTATGTTGGTGGCGAGG	240
365	Qy	GGCATCGCTCGCTCTTTCAACATGATAGCTTATAGTGATTTAGATACATTATTC	424
241	Db	GGCATCGCTCGCTCTTTCAACATGATAGCTTATAGTGATTTAGATACATTATTC	300
425	Qy	AATAAATGCACCATGTGGACAGTTCGGTGGGAGCAAGACGAGAGAGGGCCTTCCTGTAC	484
301	Db	AATAAATGCACCATGTGGACAGTTCGGTGGGAGCAAGACGAGAGAGGGCCTTCCTGTAC	360
485	Qy	CTCGCGGCTTTCTTTTCATGGACGCAATGCGATGGACCCATGCTGGCATTTCTTTAAAA	544
361	Db	CTCGCGGCTTTCTTTTCATGGACGCAATGCGATGGACCCATGCTGGCATTTCTTTAAAA	420
545	Qy	CACAAATACAGTTTCTCGTGGGATGTGCCTCAATCTCAGATGTCAATGCTCAGGTTGTT	604
421	Db	CACAAATACAGTTTCTCGTGGGATGTGCCTCAATCTCAGATGTCAATGCTCAGGTTGTT	480
605	Qy	TTTGTAGCAATTTTGCTTTCAACGTCACTGGAATGCGGGAGGCCCTGCTCATCCCGATC	664
481	Db	TTTGTAGCAATTTTGCTTTCAACGTCACTGGAATGCGGGAGGCCCTGCTCATCCCGATC	540
665	Qy	CTCTCCTTTGTATCGGGCGCATTTGCGGTGACCAACCTGCTGGCTGGCTACTACAG	724
541	Db	CTCTCCTTTGTATCGGGCGCATTTGCGGTGACCAACCTGCTGGCTGGCTACTACAG	600
725	Qy	AACATTCAGCATATCCCTGACAGAAGTGCCCGGAGCTGGGGGAGATGCAACAATA	784
601	Db	AACATTCAGCATATCCCTGACAGAAGTGCCCGGAGCTGGGGGAGATGCAACAATA	660
785	Qy	AGAAAGATGCTAGCTTCTGTGGCTTGGCTCTAATTTCTGGCCACACAGAGATCAGT	844
661	Db	AGAAAGATGCTAGCTTCTGTGGCTTGGCTCTAATTTCTGGCCACACAGAGATCAGT	719
845	Qy	CGGCTATTGTCAACCTCTTTGTTCCCGGACCTTGGTG	894
720	Db	CGTGCTATTGTCAACTCTTTGTTTCCGGGACCTTGGTG	759

RESULT 11
BU615215
LOCUS
DEFINITION
UI-H-PHO-bcg-m-04-U-I.s1 NCI CGAP FHO Homo sapiens cDNA clone
UI-H-PHO-bcg-m-04-U-I 3', mRNA sequence.
ACCESSION
BU615215
VERSION
BU615215.1 GI:23281430
KEYWORDS
EST.
SOURCE
BU615215 Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
1 (Bases 1 to 737)
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: James Martin

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
polyA=No.

FEATURES

1. Location/Qualifiers
1. .737

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443. 1179
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445. 1181
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447.
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ORIGIN

Query Match	24.5%;	Score	720.4;	DB	13;	Length	737;
Best Local Similarity	99.5%;	Pred. No.	4.3e-140;				
Matches	732;	Conservative	0;	Mismatches	3;	Indels	1;
QY	1655	TTTTGTTTGTGTTTGGTAAAGAGGGCCTTGATTTAAAGGTTTCGTGTCAATTTCTCTA	1714				
DB	2	TTTTGTTTGTGTTTGGTAAAGAGGGCCTTGATTTAAAGGTTTCGTGTCAATTTCTCTA	61				
QY	1715	GCATCTGGGTATGCTCACCTGA CGGGGGACCTAGTGAATGGTCTTTTACGTGGCTAT	1774				
DB	62	GCATCTGGGTATGCTCACCTGA CGGGGGACCTAGTGAATGGTCTTTTACTGTGGCTAT	121				
QY	1775	GTAATAAACAAACGAAACCAACTGCATTATACCCCTGCCTCAGCAAAACCCAAAGACACA	1834				
DB	122	GTAATAAACAAACGAAACCAACTGCATTATACCCCTGCCTCAGCAAAACCCAAAGACACA	181				
QY	1835	GCTGCCTCAGGTTGACGTTGTGTCCTCTCCCTGGACAATCTCCTCTTTGGAAACAAAG	1894				
DB	182	GCTGCCTCAGGTTGACGTTGTGTCCTCTCCCTGGACAATCTCCTCTTTGGAAACAAAG	241				
QY	1895	GACTGCAGCTGTGCCATCGCGCCTCGGTACCCCTGCACAGCAGGGCCACAGACTCTCCTGT	1954				
DB	242	GACTGCAGCTGTGCCATCGCGCCTCGGTACCCCTGCACAGCAGGGCCACAGACTCTCCTGT	301				
QY	1955	CCCCCTTCATCGCTCTTAAGAAATCAACAGGTTAAAACTCGGCTTCCTTTGATTTGCTTCC	2014				
DB	302	CCCCCTTCATCGCTCTTAAGAAATCAACAGGTTAAAACTCGGCTTCCTTTGATTTGCTTCC	361				
QY	2015	CAGTCACATGGCGGTACAAAGAGATGGAGCCCGGTGGCTCTTAAATTTCCCTCTTGCC	2074				
DB	362	CAGTCACATGGCGGTACAAAGAGATGGAGCCCGGTGGCTCTTAAATTTCCCTCTTGCC	421				
QY	2075	ACGGAGTTCCAAACCATCTACTCCACATGACAGAGGCGGGTGGCAGCTCAGCCCGG	2134				
DB	422	ACGGAGTTCCAAACCATCTACTCCACATGACAGAGGCGGGTGGCAGCTCAGCCCGG	481				

QY 2135 AGTCCCGGTTCCACTGAGGAACGAGACCTGTGACACACAGCAGGCTGACAGATGACAG 2194
Db 482 AGTCCCGGTTCCACTGAGGAACGAGACCTGTGACACACAGCAGGCTGACAGATGACAG 541
QY 2195 AATCTCCCGTGAAGAAGGTTGGTTTGAATGCCCCGGGGGAGCAAACTGACATGGTTGA 2254
Db 542 AATCTCCCGTGAAGAAGGTTGGTTTGAATGCCCCGGGGGAGCAAACTGACATGGTTGA 601
QY 2255 ATGATAGCATTTCACTCTGGTCTCTCTAGATCTGACAGCTGCTCAGTTCTCACCCCA 2314
Db 602 ATGATAGCATTTCACTCTGGTCTCTCTAGATCTGACAGCTGCTCAGTTCTCACCCCA 661
QY 2315 CCGT-GTATATACATGAGCTAACTTTTAAATGTCACAAAAGCGCATCTCCAGATTCC 2373
Db 662 CCGTGTATATACATGAGCTAACTTTTAAATGTCACAAAAGCGCATCTCCAGATTCC 721
QY 2374 AGACCTGCCGATGA 2389
Db 722 AGACCTGCCGATGA 737

RESULT 12
LOCUS BE876197 723 bp mRNA linear EST 20-OCT-2000
DEFINITION 601486717F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889037 5',
mRNA sequence.

ACCESSION BE876197
VERSION BE876197.1 GI:10325077
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9670 row: a column: 06
High quality sequence stop: 719.
Location/Qualifiers
1..723

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3889037"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 24.4%; Score 718.8; DB 10; Length 723;
Best Local Similarity 99.7%; Pred. No. 9.2e-140;
Matches 720; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 914 ATTATTGACGACACATCCCTGTGGTGCATGCGTACATGCGTGGTTGACGGAATCCGT 973
Db 1 ATTATTGACGACACATCCCTGTGGTGCATGCGTACATGCGTGGTTGACGGAATCCGT 60
QY 974 GCTGTGTATCTCTGCTTTCCGACGAATAAATCCCGACCAAACTCGTGTGACGACGACCAAC 1033

Db 61 GCTGTGTATCTCTGCTTTCCGACGAATAAATCCCGACCAAACTCGTGTGACGACGACCAAC 120
QY 1034 ACAGTCACGGCAGCCACATCAAGAAGTTCACTTCGCTGTCATGGCTCTGTCTCACTCAG 1093
Db 121 ACAGTCACGGCAGCCACATCAAGAAGTTCACTTCGCTGTCATGGCTCTGTCTCACTCAG 180
QY 1094 CTCTCTTTCTGTGATGTTTGGACACCCCAACGCTGTGAGAAAAATCTTGTATGACATCATC 1153
Db 181 CTCTCTTTCTGTGATGTTTGGACACCCCAACGCTGTGAGAAAAATCTTGTATGACATCATC 240
QY 1154 GGAGTGGACTTTTCCCTTTGGAGAACTCTGTGTTGTTTCCCTTGGCGATCTTCTCTCTTTC 1213
Db 241 GGAGTGGACTTTTCCCTTTGGAGAACTCTGTGTTGTTTCCCTTGGCGATCTTCTCTCTTTC 300
QY 1214 CCAGTTCCAGTTCACAGTGGGGCGCATCTCACCCGGGTGGCTGATGACACATGAGAAAAACC 1273
Db 301 CCAGTTCCAGTTCACAGTGGGGCGCATCTCACCCGGGTGGCTGATGACACATGAGAAAAACC 360
QY 1274 TTCTGCTTTGGCCCCAGCTCTGTGCTGCGGATCATCTGCTCTCATGCGCAGCCTCGTGGTC 1333
Db 361 TTCTGCTTTGGCCCCAGCTCTGTGCTGCGGATCATCTGCTCTCATGCGCAGCCTCGTGGTC 420
QY 1334 CTACCTCTACCTGGGGGTGCAGGTCGACCCCTGGGCGTGGGCTCCCTCTCTCGCGGCTTT 1393
Db 421 CTACCTCTACCTGGGGGTGCAGGTCGACCCCTGGGCGTGGGCTCCCTCTCTCGCGGCTTT 480
QY 1394 GTGGGAGAATCCACATGCTGCCATCGCTGCTGTATGCTTACCGGAAAGCAGAAAAAG 1453
Db 481 GTGGGAGAATCCACATGCTGCCATCGCTGCTGTATGCTTACCGGAAAGCAGAAAAAG 540
QY 1454 AAGATGGAGATGAGTCGCGCCACCGAGGGGAGAGCTCTGCCATGACAGATGCTCTCCG 1513
Db 541 AAGATGGAGATGAGTCGCGCCACCGAGGGGAGAGCTCTGCCATGACAGATGCTCTCCG 600
QY 1514 ACAGAGGAGGTGACAGACATCTGGAATGAGAGAGGAGAGATGAATAGGCAACGGGACGC 1573
Db 601 ACAGAGGAGGTGACAGACATCTGGAATGAGAGAGGAGAGATGAATAGGCAACGGGACGC 660
QY 1574 CATGGGCACTGCAGGAGCGGTGAGTCAGGATGACACTTCGGCATCATCTCTTCCCTCTCC 1633
Db 661 CATGGGCACTGCAGGAGCGGTGAGTCAGGATGACACTTCGGGATCATCTCTTCCCTCTCC 720
QY 1634 CA 1635
Db 721 CA 722

RESULT 13
LOCUS BQ014252/c
DEFINITION UI-H-ED1-axs-d-21-0-UI.s1 NCI CGAP ED1 Homo sapiens cDNA clone
IMAGE:3832932 3', mRNA sequence.

ACCESSION BQ014252
VERSION BQ014252.1 GI:19739153
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 732)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

JOURNAL
COMMENT

The following repetitive elements were found in this cDNA
sequence: 95-123, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5832932"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_ED1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma cell line C55. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=Chondrosarcoma
TAG_LIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"

ORIGIN

Query Match 24.4%; Score 717.4; DB 12; Length 732;
Best Local Similarity 99.3%; Pred. No. 1.8e-139; Indels 0; Gaps 0;
Matches 718; Conservative 0; Mismatches 13;

QY 2227 CCGGGGGGAGCAAACTGACATGTTGAATGATAGCATTTCACTGCGTTCTCTAGAT 2286
DB 729 CCGGGGGGAGCAAACTGACATGTTGAATGATAGCATTTCACTGCGTTCTCTAGAT 670
QY 2287 CTGAGCAAGCTGTCAGTTCTCACCCCGCCGCTGATATATACATGAGTAACTTTTAAAT 2346
DB 669 CTGAGCAAGCTGTCAGTTCTCACCCCGCCGCTGATATATACATGAGTAACTTTTAAAT 610
QY 2347 TGTCAAAAAGCGCATCTCCAGATTCAGACCCCTGCGGATGACTTTTCTGAAAGGCTTG 2406
DB 609 TGTCAAAAAGCGCATCTCCAGATTCAGACCCCTGCGGATGACTTTTCTGAAAGGCTTG 550
QY 2407 CTTTTCCTCGCTTCTCCTGAAGTTCGATAGAGGAGTCATGAGCATCTTAACCTT 2466
DB 549 CTTTTCCTCGCTTCTCCTGAAGTTCGATAGAGGAGTCATGAGCATCTTAACCTT 490
QY 2467 TGCATTTTGTGTTTTCAGTGAAGTTCAGACCCCTGCGGATGACTTTTCTGAAAGGCTTG 2526
DB 489 TGCATTTTGTGTTTTCAGTGAAGTTCAGACCCCTGCGGATGACTTTTCTGAAAGGCTTG 430
QY 2527 GTTCTGTAGGGTAACTTTTGAAGTAGATATATPACCTGTTTCTGCTATCCTTAGTCATA 2586
DB 429 GTTCTGTAGGGTAACTTTTGAAGTAGATATATPACCTGTTTCTGCTATCCTTAGTCATA 370
QY 2587 ACTTCGGGTACAGTAATGAGATGCTACGATGTTTCCCTCCACACCATAGATATA 2646
DB 369 ACTTCGGGTACAGTAATGAGATGCTACGATGTTTCCCTCCACACCATAGATATA 310
QY 2647 AAGCAAGACATTTTATAACGATACAGAGTCACATATGTGTCTCTCTGAAATAAGCAT 2706
DB 309 AAGCAAGACATTTTATAACGATACAGAGTCACATATGTGTCTCTCTGAAATAAGCAT 250
QY 2707 TCGAAATCCATGCGATGAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTCCTTTA 2766
DB 249 TCGAAATCCATGCGATGAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTCCTTTA 190

QY 2767 AAAAAATTATACACACGGTTCTACTAAATTTGATTTAGTTCAGAAATTCCTAGACTGAAAGAAC 2826
DB 189 AAAAAATTATACACACGGTTCTACTAAATTTGATTTAGTTCAGAAATTCCTAGACTGAAAGAAC 130
QY 2827 CTAACAAAAAATAATTTTAAAGATATAATAATATATGCTGCTATATGTTATGTTATTTT 2886
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QY 2887 TAGGCTATATACATTTCTCTATTTTCGCATTTTTCATATAAAATGCTCTATATACAAAAA 2945
DB 69 TAGGCTATATACATTTCTCTATTTTCGCATTTTTCATATAAAATGCTCTATATACAAAAA 11

RESULT 14

BQ009716/c
LOCUS BQ009716 729 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-ED0-aya-d-17-0-UI-si NCI_CGAP_ED0 Homo sapiens cDNA clone
IMAGS:5836000 3', mRNA sequence.
ACCESSION BQ009716
VERSION BQ009716.1 GI:19734617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 95-123, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
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/clone="IMAGE:5836000"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED0"
/note="Organ: Left Pubic Bone; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_ED0 is a cDNA library containing the following tissue(s): Chondrosarcoma cell line C55. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=Chondrosarcoma
TAG_LIB=UI-H-ED0
TAG_SEQ=CGTCAAGGCT"

ORIGIN

Query Match 24.3%; Score 717; DB 12; Length 729;
Best Local Similarity 99.7%; Pred. No. 2.2e-139;

Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy 2227	CCGGGGGCGACAACTGACATGGTTGAATGATAGATTTCACTGCGCTTCTCTAGAT 2286
Db 729	CCGGGGGCGACAACTGACATGGTTGAATGATAGATTTCACTGCGCTTCTCTAGAT 670
Qy 2287	CTGAGCAAGCTGTGCTCCTCACCCCGGCTGTATATACATGAGCTAACTTTTAAAT 2346
Db 669	CTGAGCAAGCTGTGCTCCTCACCCCGGCTGTATATACATGAGCTAACTTTTAAAT 610
Qy 2347	TGTCACAAAGCGCATCTCCAGATTCAGACCCCTGCCGCGATGACTTTCTGAGCGCTTG 2406
Db 609	TGTCACAAAGCGCATCTCCAGATTCAGACCCCTGCCGCGATGACTTTCTGAGCGCTTG 550
Qy 2407	CTTTTCCCTCGCCTTCTCGAAGTGCATTTAGAGCGAGTCACATGGAGCATCTTAACIT 2466
Db 549	CTTTTCCCTCGCCTTCTCGAAGTGCATTTAGAGCGAGTCACATGGAGCATCTTAACIT 490
Qy 2467	TGCATTTTGTGTTTACAGTGAATGAGCTTTTAACTCTCATCCAGCATCTTAATGCCAG 2526
Db 489	TGCATTTTGTGTTTACAGTGAATGAGCTTTTAACTCTCATCCAGCATCTTAATGCCAG 430
Qy 2527	GTTCGTGAGGTTAACTTTTGAAGTAGATATATTACCTGGTTCTGCTATCTTATGTCATA 2586
Db 429	GTTCGTGAGGTTAACTTTTGAAGTAGATATATTACCTGGTTCTGCTATCTTATGTCATA 370
Qy 2587	ACTTCGCGGTACAGTAATGAGAACTGACGCTTCTCCCTCCACACCATACGATA 2646
Db 369	ACTTCGCGGTACAGTAATGAGAACTGACGCTTCTCCCTCCACACCATACGATA 310
Qy 2647	RAGCAAGACATTTTATACGATACAGAGTCACATGTTGTCCTCCCTGAAATAACGCAT 2706
Db 309	RAGCAAGACATTTTATACGATACAGAGTCACATGTTGTCCTCCCTGAAATAACGCAT 250
Qy 2707	TGCAATCCATGCACTGAGTATATTTTCTAAGTTTGAAGAGCAGGTTTTTCTTTTA 2766
Db 249	TGCAATCCATGCACTGAGTATATTTTCTAAGTTTGAAGAGCAGGTTTTTCTTTTA 190
Qy 2767	AAAAATATACACGCTTCACTAAATGATTAGTCAGATTCCTAGACTGAAAGAAC 2826
Db 189	AAAAATATACACGCTTCACTAAATGATTAGTCAGATTCCTAGACTGAAAGAAC 130
Qy 2827	CTAAACAAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTT 2886
Db 129	CTAAACAAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTT 70
Qy 2887	TAGGCTATATACATTCCTATTTTTCGATTTTCAATAAATGCTCTTAATACAAAAA 2945
Db 69	TAGGCTATATACATTCCTATTTTTCGATTTTCAATAAATGCTCTTAATACAAAAA 11
RESULT 15	
CB241863/C	
LOCUS 726 bp mRNA linear EST 12-FEB-2003	
DEFINITION UI-CF-FNO-aga-i-07-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone	
ACCESSION CB241863	
VERSION CB241863.1	
KEYWORDS GI:28363507	
SOURCE EST.	
ORGANISM Homo sapiens (human)	
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS Bonaldo.M.F., Lennon.G. and Soares.M.B.	
TITLE Normalization and subtraction: two approaches to facilitate gene discovery	
JOURNAL Genome Res. 6 (9), 791-806 (1996)	
MEDLINE 9704477	
PUBMED 8889548	
COMMENT Contact: McCray, PB	
McCray Lab	
University of Iowa	

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA	
Tel: 319 356 4866	
Fax: 319 356 7171	
Email: paul-mccray@uiowa.edu	
Tissue Procurement: Dr. M. J. Welsh, University of Iowa	
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa	
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).	
The following repetitive elements were found in this cDNA sequence: 95-123, >AT rich#Low_complexity (matched complement)	
Seq primer: M13 FORWARD	
POLYA=Yes.	
Location/Qualifiers	
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/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="UI-CF-FNO-aga-i-07-0-UI"	
/tissue_type="Human Lung Epithelial cells"	
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"	
/clone_lib="UI-CF-FNO"	
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DUI). The library was subtracted according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu	
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS	
6hr to LPS 24h	
TAG LIB=UI-CF-FNO	
TAG_SEQ=CTGCTCAGGT"	
ORIGIN	
Query Match 24.3%; Score 715; DB 14; Length 726;	
Best Local Similarity 100.0%; Pred. No. 5.8e-139;	
Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2231	GGGGGAGCAAACTGACATGGTTGAATGATAGATTTCACTGCGCTTCTCTAGATCTGA 2290
Db 725	GGGGGAGCAAACTGACATGGTTGAATGATAGATTTCACTGCGCTTCTCTAGATCTGA 666
Qy 2291	GCAAGCTGTGCTCTCACCCCCCAGCTGTATATACATGAGCTAACTTTTAAATTTGTC 2350
Db 665	GCAAGCTGTGCTCTCACCCCCCAGCTGTATATACATGAGCTAACTTTTAAATTTGTC 606
Qy 2351	ACAAAAGCGCATCTCCAGATTCAGACCCCTGCCGATGACTTTTCTGAGCGCTTCTTT 2410
Db 605	ACAAAAGCGCATCTCCAGATTCAGACCCCTGCCGATGACTTTTCTGAGCGCTTCTTT 546
Qy 2411	TCCTCGCCTTTCTGAGGTCGCAATTAGAGCGAGTCACATGAGCATCTTAACTTTGA 2470
Db 545	TCCTCGCCTTTCTGAGGTCGCAATTAGAGCGAGTCACATGAGCATCTTAACTTTGA 486
Qy 2471	TTTTAGTTTTTACAGTGAAGCTTAAAGTCTCATCCAGCATTTCTAATGCCAGTTG 2530
Db 485	TTTTAGTTTTTACAGTGAAGCTTAAAGTCTCATCCAGCATTTCTAATGCCAGTTG 426
Qy 2531	CTGTAGGTAACCTTTTGAAGTACATATATTACCTGGTTCTGCTATCTTCTAGTCATAACTC 2590
Db 425	CTGTAGGTAACCTTTTGAAGTACATATATTACCTGGTTCTGCTATCTTCTAGTCATAACTC 366
Qy 2591	TGCGGTACAGGTAATTGAGAAATGTACTACGGTACTTCCCTCCACACCATACGATAAGC 2650
Db 365	TGCGGTACAGGTAATTGAGAAATGTACTACGGTACTTCCCTCCACACCATACGATAAGC 306
Qy 2651	AAAGCATTTTATACGATACAGGTCACATGTGTTCTCTCCCTCCCTGAAATACGATTCGA 2710
Db 305	AAAGCATTTTATACGATACAGGTCACATGTGTTCTCTCCCTGAAATACGATTCGA 246

QY	2711	ATCCATGCGTGCAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTTCCTTTAAAAA	2770
Db	245	ATCCATGCGTGCAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTTCCTTTAAAAA	186
QY	2771	AATTATAGACACGGTTTCACTAAATTGATTAGTCAGAATTCCTAGACTGAAAGAACCTAA	2830
Db	185	AATTATAGACACGGTTTCACTAAATTGATTAGTCAGAATTCCTAGACTGAAAGAACCTAA	126
QY	2831	ACAAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTATATTTTAGG	2890
Db	125	ACAAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTATATTTTAGG	66
QY	2891	CTATAATACATTTCCCTATTTTTCGCAATTTCAATAAAATGCTCTAATACAAAAA	2945
Db	65	CTATAATACATTTCCCTATTTTTCGCAATTTCAATAAAATGCTCTAATACAAAAA	11

Search completed: April 25, 2004, 19:28:04
Job time : 7366 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:53:44 ; Search time 46 Seconds
(without alignments)
3374.673 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527
Sequence: 1 MVKFPALHYWPLRFLVPL.....TDMPTTEVTDIVEMRSENE 492

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp archaea.*
- 2: sp bacteria.*
- 3: sp fungi.*
- 4: sp human.*
- 5: sp invertebrate.*
- 6: sp mammal.*
- 7: sp mhc.*
- 8: sp organelle.*
- 9: sp phase.*
- 10: sp plant.*
- 11: sp rodent.*
- 12: sp virus.*
- 13: sp vertebrate.*
- 14: sp unclassified.*
- 15: sp rvirus.*
- 16: sp bacteriap.*
- 17: sp archaep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2479	98.1	492	11 Q8C438	Q8C438 mus musculus
2	183.5	7.3	449	16 Q8YXP4	Q8YXP4 anabaena sp
3	180.5	7.1	453	16 Q8ZSC4	Q8ZSC4 anabaena sp
4	138	5.5	455	16 Q8XHF0	Q8XHF0 clostridium
5	121.5	4.8	474	2 Q9RHD4	Q9RHD4 pseudomonas
6	119.5	4.7	593	16 Q9JYN9	Q9JYN9 neisseria m
7	118.5	4.7	462	17 Q96YE7	Q96YE7 sulfolobus
8	118.5	4.7	490	17 Q8THQ1	Q8THQ1 methanosaarc
9	117.5	4.6	511	16 Q8CNP2	Q8CNP2 staphylococ
10	117.5	4.6	693	16 Q9JTN5	Q9JTN5 neisseria m
11	117	4.6	450	16 Q8XT07	Q8XT07 ralsfontia s
12	117	4.6	469	16 Q81F82	Q81F82 bacillus ce
13	117	4.6	481	2 Q9RQG9	Q9RQG9 streptococc
14	117	4.6	481	2 Q07870	Q07870 streptococc
15	117	4.6	535	6 Q9N1Q4	Q9N1Q4 oryctolagus
16	116.5	4.6	529	13 Q7ZWV7	Q7ZWV7 xenopus lae

17	115.5	4.6	670	8	O21285	O21285 reclinomona
18	115.5	4.6	784	16	Q8KDB0	Q8KDB0 chlorobium
19	115	4.6	444	16	Q8Y9Z4	Q8Y9Z4 listeria mo
20	115	4.6	507	16	Q8K9E2	Q8K9E2 bacillus ha
21	114.5	4.5	447	17	Q28801	Q28801 archaeglob
22	114.5	4.5	547	16	Q879H7	Q879H7 streptococc
23	114	4.5	542	16	Q8K673	Q8K673 streptococc
24	113.5	4.5	512	16	Q99SY5	Q99SY5 staphylococ
25	112.5	4.5	398	16	Q8Z4K9	Q8Z4K9 salmonella
26	112.5	4.5	488	16	Q891V9	Q891V9 clostridium
27	112.5	4.5	497	2	Q30986	Q30986 staphylococ
28	112	4.4	461	17	Q8U2X0	Q8U2X0 pyrococcus
29	111.5	4.4	559	16	Q8PJ2	Q8PJ2 xanthomonas
30	111	4.4	475	16	Q88XM1	Q88XM1 lactobacill
31	111	4.4	542	16	Q99Y06	Q99Y06 streptococc
32	111	4.4	556	16	Q8NZX7	Q8NZX7 streptococc
33	111	4.4	582	16	Q81F44	Q81F44 bacillus ce
34	110.5	4.4	400	16	Q8Z407	Q8Z407 salmonella
35	110.5	4.4	452	16	Q92FS0	Q92FS0 listeria in
36	110.5	4.4	826	16	Q88I00	Q88I00 pseudomonas
37	110	4.4	450	16	Q8E3W6	Q8E3W6 streptococc
38	110	4.4	599	10	Q7X9X8	Q7X9X8 plantago ma
39	109.5	4.3	400	16	Q8ZVA5	Q8ZVA5 salmonella
40	109.5	4.3	427	16	Q8KSI1	Q8KSI1 vibrio chol
41	109	4.3	412	16	Q88WH5	Q88WH5 lactobacill
42	109	4.3	450	16	Q8DYAL	Q8DYAL streptococc
43	109	4.3	494	16	Q8KCP9	Q8KCP9 chlorobium
44	109	4.3	552	16	Q886F5	Q886F5 pseudomonas
45	108.5	4.3	450	16	Q8YAS9	Q8YAS9 listeria mo

ALIGNMENTS

RESULT 1

Q8C438	PRELIMINARY;	PRT;	492 AA.
ID	Q8C438		
AC	Q8C438;		
DT	01-MAR-2003 (Tremblrel. 23, Created)		
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)		
DE	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	Progressive ankylosis.		
GN	ANK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=hippocampus;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RL	Nature 420:563-573(2002).		
DR	EMBL; AK083135; BAC38778.1; -		
DR	MGD; MGI:86023; ank.		
DR	GO; GO:0005887; C:integral to plasma membrane; IDA.		
DR	GO; GO:0007626; P:locomotory behavior; IMP.		
DR	GO; GO:0001501; P:skeletal development; IMP.		
SQ	SEQUENCE 492 AA; 54336 MW; 6923EA3A85D0BDC CRC64;		
Query Match	98.1%; Score 2479; DB 11; Length 492;		
Best Local Similarity	97.8%; Pred. No. 1.6e-203;		
Matches 481; Conservative	5; Mismatches 6; Indels 0; Gaps 0;		
Oy	1 MVKFPALHYWPLRFLVPLGITNIAIDFGFQALNRSIGIAVKEDAVEMLASGLVSLMK 60		
Db	1 MVKFPALHYWPLRFLVPLGITNIAIDFGFQALNRSIGIAVKEDAVEMLASGLVSLMK 60		
Oy	61 FFTGPMSEDFKNVGLVFNVNSKRDRTKAVLCMVVAGAIAAVPHTLIAYSDIGYIINKLHV 120		

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Db 61 FFTGPMDSFKNVGLVFNVRKDRKAVLQVWVAGIAAFTHTIAVSDLGYYIINKLHV 120
Qy 121 DESVGSKTRRAFLYLAAPFPDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVGSKTRRAFLYLAAPFPDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
Qy 181 HSHLECEPLLPILSLYMGALVRCCTTLCGLGYKNHDIIPDRSGPELGGDATIRKWSF 240
Db 181 HSHLECEPLLPILSLYMGALVRCCTTLCGLGYKNHDIIPDRSGPELGGDATIRKWSF 240
Qy 241 WPLALILATORISRPVNLVFSRDLGSSAAEAVAILTATVPVGHMPPGWLTEIRAVY 300
Db 241 WPLALILATORISRPVNLVFSRDLGSSAAEAVAILTATVPVGHMPPGWLTEIRAVY 300
Qy 301 PAFKNNPSKLVSTNTVTAHHKFTFVCMALSLTLCFVMTWPNVSKILLIDIIGVD 360
Db 301 PAFKNNPSKLVSTNTVTAHHKFTFVCMALSLTLCFVMTWPNVSKILLIDIIGVD 360
Qy 361 FAFELCVPLRIEFPFPVTVRAHLLTGLMTLTKTFFVLAPSRLIIVLISLVLPY 420
Db 361 FAFELCVPLRIEFPFPVTVRAHLLTGLMTLTKTFFVLAPSRLIIVLISLVLPY 420
Qy 421 LGVHGATLGVGSLLAGFVGSTWVAIAACVYVRKQKKMENESATEGEDSAMTMPTEE 480
Db 421 LGVHGATLGVGSLLAGFVGSTWVAIAACVYVRKQKKMENESATEGEDSAMTMPTEE 480
Qy 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492

RESULT 2
Q8YXP4 PRELIMINARY; PRT; 449 AA.
AC Q8YXP4;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Hypothetical protein A111168.
GN A111168.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2159285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003584; BAB73125.1; -.
DR PIR; AE1952;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 449 AA; 49860 MW; F5841D2C21CC82D5 CRC64;

Query Match 7.3%; Score 183.5; DB 16; Length 449;
Best Local Similarity 21.0%; Pred. No. 3.5e-07;
Matches 97; Conservative 92; Mismatches 201; Indels 71; Gaps 14;

Qy 13 LIRFVLPLGINTIADFGCE---QALNRGIAAVKEDAVEMLASVGLAYSLMKPFTGPMDS 68
Db 25 LITQFIPUSLSDVAMTLGDPLOTGALSRL--LAFQ---ETLAGVGVKGVAVFLESFIIM 79
Qy 69 FKNVGLFVNSKRDRTKAVLCWVAGIAAFTHTIAVSDLGYYIINKLHVDESVGSKT 128
Db 80 ILHASTALGGQAKSRRLAQVTFVLSGIFFLLTWEPLYNLLDVFVSSLIARQ 139
Qy 129 RFAFLYLAAPFPDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLE 188
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Db 140 RTAFLLMFWPFVIAWRRFQGLLIRAQKSIAGWASVARLTWVVSLSLVGVNURLDGM 199
Qy 189 PLLIPILSLYMGALVRCCTTLCGLGYKNHDIIPDRSGP---ELGGDATIRKM-----L 238
Db 200 LAGITWMAAILLEAVLTWFCGL-----RLGAISILEQGYSETKKLPQTLSGV 247
Qy 239 SFWW-PLALILATORISRPVNLVFSRDLGSSAAEAVAILTATVPVGHMPPGWLTEI- 296
Db 248 SFYFLPLASTMLIVNGARAILLSIARSDGSL-----ALAVNPAT-----WGLLSIA 296
Qy 297 -----RAVPAFAPKNNPSKLVSTNTVTAHHKFTFVCMALSLTLCFVMTWPNVS 349
Db 297 NGRMIQVVISAYEE-----TSRTLAAFV-----IIVGLSFTLIPFELGFTDQG 342
Qy 350 EKILIDIVGDPAPAFELCVPLRIEFPFPVTVRAHLLTGLMTLTKTFFVLAPSRL- 407
Db 343 LFLRQFTLGNPNSLVEASRPVLIQSLCPFLALQNTFQGLLIHKGNWFINLATVVAAT 402
Qy 408 -IIVLIASLVLPYLGVHGATLGVGSLLAGFVGSTWVAIA 447
Db 403 FLIVICGSLIFTKHSGATSAAYG---MLAGVNSEIIVFLA 440

RESULT 3
Q8ZSC4 PRELIMINARY; PRT; 453 AA.
AC Q8ZSC4;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Hypothetical protein A1R7587.
GN A1R7587.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2159285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003602; BAB77230.1; -.
DR PIR; AH2537; AH2537.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 453 AA; 49289 MW; 5E9337F924EE9B87 CRC64;

Query Match 7.1%; Score 180.5; DB 16; Length 453;
Best Local Similarity 20.4%; Pred. No. 6.4e-07;
Matches 94; Conservative 91; Mismatches 206; Indels 69; Gaps 15;

Qy 13 LIRFVLPLGINTIADFGCEQALNRGIAAVKEDAVEMLASVGLAYSLMKPFTGPMDSFKNV 72
Db 34 LUKQFIPUSLSDVAMTLGDPLOTGALSRLSPFQ-ETLAGVGVKGVAVFLESFIIMILHA 92
Qy 73 GLVFNKSRDRTKAVLCWVAG-ALAAVFHTLIAVSDLGYYIINKLHVDESVGSKTERR 131
Db 93 STALGQAKSRRLVQVTFVIAGLALSGIP-LFLTWKPLYNLLDLFGVSSSIAARGRTA 151
Qy 132 FLYLAAPFPDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLE----- 185
Db 152 FLIMLWPFVIAWRRFQGLLIRAHSKSIAGWASVARLTWVVSLSLVGVNURLDGAFLAG 211
Qy 186 -----CREPLIPILSLYMGALVRCCTTLCGLGYKNHDIIPDRSGPELGGDATIRKWL 238
Db 212 ITWMAAILLEAVLTWFCGLGALISILNQ--QGYSET-----KKLPQTGEVTF---- 258
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QY 239 SFWWPLALILATQRI SRPIVNL FVSRDLGGSSAATEAVAILTATYPUGHMPYGMLETI-- 296
Db 259 -YFLPLASTMLLVWGARAILLSLIARAFDGS-----IALVWPAA---WGLLSLIAN 306
QY 297 -----BAVYPADFKNPNKLVSTNTVTAHHKKFTFCVCMALSLTLCFVWFMTNPNVSE 350
Db 307 GTRMTQQVVISAYEE-----TSRRTLAFAV-----IIVGLSFTLIPFLGYTDQGL 352
QY 351 KILIDIIGVDFAPAECLVVPPLRIFFPFVTVRAHLTGWLMTL-KKTFVLAPSSVLR-- 409
Db 353 FLTROFLGNPNLSVNASREVIQILSCLPLLLALQNTFQGLLTHGKNWFINLATLVAAIL 412
QY 410 VLI--ASLVLPVLGVHGATLGVGSLAGFVGSWTVAIA 447
Db 413 TLVVGCTLFTRHSGANSAYG---MLAGVIGELIIVLFFA 449

RESULT 4
QBXHR0 PRELIMINARY; PRT; 455 AA.
AC QBXHR0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein CPE2535.
GN CPE2535.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohkani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayaashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003194; BAB82241.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR TIGRFAMs; TIGR00797; mate; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 455 AA; 48384 MW; A564CC4F22PBD059 CRC64;

Query Match 5.5%; Score 138; DB 16; Length 455;
Best Local Similarity 21.0%; Pred. No. 0.0028;
Matches 97; Conservative 82; Mismatches 190; Indels 94; Gaps 19;

QY 17 LVPLGIT-NIAIDFGEQALNRGIAAVKEDAVEMLASGLAYSLMKFTGPMSPDKNVLV 75
Db 71 LIGIGATANISIKGQNK-----RKDAKILGNSVLTITSLV-----LTIVGIV 116
QY 76 FVNSKDRTRKAVLCWVAGAAVAFHTLIAYSDLGYYIINKLHHVDESVSCKTRAPLYL 135
Db 117 FANS-----ILHLFGASEATIFY---AKYINVLILGTIFNLMSFSLYSTIRA---- 161
QY 136 AAFPPMDAMANTHAGILLKHKYSFLVGCASISDVIAQVFAILLHLHLECRPEPLIPI 195
Db 162 DGNFMSAAV-----WVLGC--IINVLDAVFIVP---NLGIKGAALATVI 203
QY 196 SLYMGALVRCCTLCGLGYKNIHDIIPDRSGPELGGDATIRKMSF---WHPALAILA--- 249
Db 204 SQIV-----TTLIMLYYTT-----LGSNKLKLFETKLDLWRLVIVLAIGV 245
QY 250 ---TORISRPVNLVFSRDLG--QSSATEAVAILTATYPUGHMPYGMLETIRAVYPAFD 304
Db 246 APTSQMAASVVQVIANNALRWYGGDLAIGAWAAISSAMIFLMPITGNO--GSQFIIG 303

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QY 305 KKNPSKNLYSTNTVTAHHKKFTFCVCMALSLTLCFVWFMTNPNVSEKILIDIIGVDFAF 364
Db 304 YNTGAKYERAKTIVKLAIAATITIVLGILLQAF-----PALVISMENSDPKLL 354
QY 365 ELCVPLRIFSPFPVTVRAHLTGWLMTLKKTFVLAPSSVLR--IIVLIASLVVLYLGV 423
Db 355 EIGVPLRIYLFVWPIIGISIIIGSNYFQSIGKAKLATFLSLRQVILLITPLTIVLPKIA 414
QY 424 HGATLGVGSLAGFVGSWTVAIAACVYVRKOKKK--MENESA 464
Db 415 IGLT---GWLAGTVSDFLSTITGLFIKEFKKEDSIEDEKA 454

RESULT 5
QBHRD4 PRELIMINARY; PRT; 474 AA.
AC QBHRD4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wzx (Similar to polysaccharide biosynthesis protein).
GN WZX.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IATS O6;
RX MEDLINE=20090474; PubMed=10627048;
RA Belanger M., Burrows L.J., Lam J.S.;
RT "Functional analysis of genes responsible for the synthesis of the B-
RT band O antigen of Pseudomonas aeruginosa serotype O6
RT lipopolysaccharide.";
RL Microbiology 145:3505-3521(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22053227; PubMed=12057956;
RA Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavin T.V.,
RA Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
RT "Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas
RT aeruginosa.";
RL J. Bacteriol. 184:3614-3622(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=2-164;
RA Burns J., Kaul R., Olson M.;
RT "Whole Genome Sequence Variation Among Multiple Isolates of Pseudomonas
RT aeruginosa.";
RL J. Bacteriol. 0:0-0(2003).
DR EMBL; AF035937; AAF24000.1; -.
DR EMBL; AF498417; AAM27819.1; -.
DR EMBL; AF540991; AAO17416.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc synt.
DR Pfam; PF01943; Polysacc synt; 1.
SQ SEQUENCE 474 AA; 51401 MW; C867BC84B086E1B6 CRC64;

Query Match 4.8%; Score 121.5; DB 2; Length 474;
Best Local Similarity 20.3%; Pred. No. 0.075;
Matches 89; Conservative 75; Mismatches 174; Indels 101; Gaps 21;

QY 48 MLASGLAYSLMKFTGPMSPDKNVL-VFVN--SKDRTRKAVLCWVAGAAVAFHTLI 104
Db 1 MLGKSLVYFLFKSPAILT---LVGLSVFTLLSPGEGVYSLIIVVGLNTVFLQWV 57
QY 105 AYSDLGYYIINKLHHVDESVSCK---TRAPLYLAAP--FMDAMAW---THAGI-LLKH 155
Db 58 ALG-VGRYL---PECSDDQARALLGTARAIISFLVSLIIVFTFLWREMBIGSILY 113

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156 KYSFLVGCASISD-----VIAQVVFVAILHSHLEPRELLIPILSYMG----- 200
114 MVGFLCLAQWHLNLKIONAILQPLTYGKMLL---IKGAGSFFIGVLLVYFGVGDGLL 170
201 -----ALVRCCTTLCGLGYKXNHDIIPRSGPELGGDATIRKMLSEFWPLALILATQISR 255
171 LGTVLSVLATITFQDAWRGVSVALDKR-----QLTRLFAYGAPLTLTFLFAFYVN 222
256 PIVNLFYSRDIGSSAATAEAVAILTATYPVG-----HMPYGMWLTETRAYVPAPDKNPS 309
223 ASDRFFIGAFGLGDAAGVSVSYDLAQVSGVTASVVHL-----AAFLVMKLSK 273
310 NKIVSTNTVTAHIKFTFCVMALSLTLCFWMFTNVSEKILIDIIGVDEFAFAELCVV 369
274 SGLPQTDQLR-----KTIFIFAVVSPACGLAWVAEISGSIN-----GEEFREGALKII 325
370 PLRIFSPFPVTVRAHLTGLWMTIKK-----TFVLAPSSVLRILVLIAS-----LV 416
326 PL-----ISLSAFLGALKSPFYDYSFQLASATRVQVTVAVSAVVDWENLI 372
417 VLPYLGVGHGALGVGSLLA 435
373 LIPEFGIVGA--AVSSVMA 389

RESULT 6
Q9JYN9 PRELIMINARY; PRT; 693 AA.
AC Q9JYN9;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Carbon starvation protein A.
GN NMB1493
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Feden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
RA "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL; AE002498; AAP41849.1; -.
DR PIR; C81078; C81078.
DR TIGR; NMB1493; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009267; P:cellular response to starvation; IEA.
DR InterPro; IPR003706; CstA.
DR Pfam; PF02554; CstA; 1.
KW Complete proteome.
SQ SEQUENCE 693 AA; 74518 MW; A315785B6985DC0 CRC64;

Query Match 4.7%; Score 119.5; DB 16; Length 693;
Best Local Similarity 22.2%; Pred. No. 0.18; Indels 139; Gaps 26;
Matches 111; Conservative 69; Mismatches 181; Indels 139; Gaps 26;

QY 12 PLIRFLVPLGTTINIAIDFGS-QALNRGIAAVKSDAVEMLASGLAYSLMKFFTPGMSDPK 70
DB 270 PVMLLTPRDVLSLFTLGIATIALALGIVV-NPALQMPAVTHFDGSGVFSGLAFPE- 327
QY 71 NVGLVFNKSDRTKAVLCMVVGAIAAVFHTLIAYSDLGYYINKLHVDESVSQKTR 130

328 -----LPI-----TIACGAVSG-----PHALISGTTPKOLENETHVRMIGYGMIME 370
131 AFLYLAAFPFMDAMWTHAGI-LLKHKYSFLVGCASISDVIAQV-----VFVAILLH 181
371 SFVAIMA---LAAASLDPGVYFAXNSPALIG---TDANTAAEVITTKLQFPDAAIILH 425
182 SHLECREPLILPILSLYMGALVRCCTTLCGLGYKXNHDIIPRSGPELGGDATIRKMLSFV 241
426 TAKEVGEN---TILSRAGA---PTLAVGMAHIMSLIP-----GEA---MMAFW 466
242 WPLAIL-----ATQISRPVNLVFSRDLGG-----SSAATEAVAILTAT 282
467 VHFALLFEALFILTAVDAGTRVAR-----FMQDLGSIIFYKPFNGTDSIPANLIATFFAV 521
283 YPVGHPMPYGMWLT-----IRAVYPAFDKKNPSKNLSTNTVTAHIKFTFCVMALSLT 338
522 ALWNGFLYTGVTDPGLGINSWPLP-----GIANQMLA-----GVALIM 560
339 CFVWF-----WTPNVSEKILIDIIGVDEFAFAELCVVPLRIFSPFPVTVRAHLTG 389
561 CAVVLIKMKRDYVWV-----VLVPAVGVLV-----TCYAGLOKLFHSDPRISFHAHAK 611
390 WLMTKTKTFVLAPS-----SVLRIL-----VLIASLVLPYLGVGHGALGVGSLLA 435
612 YSDALAKNEILAPAKDIGEMAQIIFNDKINAGLTILFLSVVVI---VAAYGLRT---ALKA 666
436 GFVGESTMVAAIACVYVRKQ 455
667 RKVGWPTAKEIPAVYVRGKQ 686

RESULT 7
Q96YE7 PRELIMINARY; PRT; 462 AA.
AC Q96YE7;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative NADH-plastoquinone oxidoreductase subunit 2.
GN S12223.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RA "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7."
RL DNA Res. 8:123-140(2001).
DR EMBL; AF000989; BAB67330.1; -.
DR GO; GO:0008137; P:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u...; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001750; Oxidored_gi.
DR Pfam; PF00361; oxidored gi; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMWA; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 462 AA; 50002 MW; E99457D221AE3892 CRC64;

Query Match 4.7%; Score 118.5; DB 17; Length 462;
Best Local Similarity 19.0%; Pred. No. 0.13; Indels 127; Gaps 18;
Matches 82; Conservative 78; Mismatches 145; Indels 127; Gaps 18;

QY 69 FKVGVLVFNKSDRTKAVLCMVVGA-GAIAAVFHTLIAYSDLGYYINKLHVDESVSQK 127

Db 17 PSSIAVLIDN-GRSRYIIADVLSIGTLVSLFLTLIFVGLGY------GYS 63
 QY 128 TRAFLYIAAPFMDAMWTHAGILLKHKYSLVCCASISDVIAQVFAVAILLHSHLECR 187
 Db 64 LFSSTLYLSNFGYFIA-----VSAILATI-----IVVGGMESL 97
 QY 188 EPLLIPILSLVGLVRCCTTLCLGYKNIHDIIPDRSGPELGGDATIRKMLSFWMPLALI 247
 Db 98 EPIKTRSFSLAMLTDLGVIVLGFAYSVIT-----LASM----- 133
 QY 248 LATQIRSPVNLVFSRDLGGSSAATEAVAILTATYP-----VGMPPYGWITERAV--Y 300
 Db 134 -----GIASATYVIAMIRKDYSTIAGVKYLINGLLSSLSMLVLGF 174
 QY 301 PAFDKNPNKLVSTNTVTAAHIKFTFVCMALSLTLCF-----VNFWTNPV---SEK 351
 Db 175 AFFILIGLSLDATINVTQTLVILG-----INFLSIAFLFKVGAFFQAWLPDYVMSDR 229
 QY 352 ILI-----DIIGVDFAFALC-----VPLRIPSPFPVPTVRAHLTGWMLTKK-- 396
 Db 230 ISVAFVSSVGKIVGAPLFDIIFLYPKSGIVGFSIFVIFAL-ITVMSLIFGNIVAFSRQD 288
 QY 397 -TFVLAPSSVLRIIVLIASLVLPYLVGHGATLGVGSLLAGFVGBSTWVAIAACYVRKQ 455
 Db 289 FASMLAYSSITQVGFMLIAITMLPY-----NPIVSTSGMLVYLAYS--IAQAGLFIALSH 342
 QY 456 KKKMENESATEG 467
 Db 343 IEKVSGTSVIEG 354

RESULT 8

ID Q8THQ1 PRELIMINARY; PRT; 490 AA.
 AC Q8THQ1
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Polysaccharide biosynthesis protein.
 GN MA4461.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=19322238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atncor D., Brown A.,
 RA Allen N., Naylor J., Spang-Thomann N., Dearellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hederich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Unway L.F., White O., White R.H., de Macario E.C.,
 RA Feary J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett N., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity."
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AE011167; AAM07802.1; .
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
 DR InterPro; IPR002797; Polysacc_synt.
 DR Pfam; PF01943; Polysacc_synt; 1.
 KW Complete proteome.
 SQ SEQUENCE 490 AA; 54715 MW; 03E2B2A3A9A0DB1 CRC64;

Query Match 4.7%; Score 118.5; DB 17; Length 490;
 Best Local Similarity 22.1%; Pred. No. 0.14;
 Matches 105; Conservative 82; Mismatches 158; Indels 131; Gaps 26;

QY 16 FLVPLGITNI--AIDFGEQA-LNRGIAAVKEDAVEMLASYGLAYSIMKFFTPGMSDFKNV 72
 Db 27 FLPLV-ITKLGAYDGIWAQIN-----ITVSLVSPALMGLMSPIR----- 68
 QY 73 GLVFNKSDRTRKAVLCMVVAGNAIAVFTLAYSDLGYIINKLHHVDESVGSKTRRAF 132
 Db 69 ---FLSETEKKK-----IREVVYSILFFVTVGFLASSLLYVFAEP----- 107
 QY 133 LYLAAFPFMDAMA--WTHAGILLKHKYSLVLCASISDVIAQVFAVAILLHSHLECR-- 188
 Db 108 --LATGFQDPSATYFVQAGSL-----IFLVIESIS-LFYPRVPRQIKKFSYFTLFTF 160
 QY 189 -PLLIPILSYNG-----ALVRCITCLG-----YKNIHDIIPDRSGPELGGDATI 234
 Db 161 GKLLFTLFLFNGYGLGVITATLAVQGLIFLAFVTVISQIGFVPOFT-----CI 212
 QY 235 RKMLSFWMLA---LILATQIRSRPVLNLFVSRDLGGSSAATEAVAILTATYPVGHMPY 290
 Db 213 REHLQSLPLTPNVLNLTWDSSDRYNTVYFLG--LG-----SVGVSAACSIGNLIQ 263
 QY 291 GMLTEIRAV-YP---AFDQNPNSKLVSTNSVTAAHIKKFTFVCM-----ALSLTL 338
 Db 264 LFVSPQLILFPELSKLFDENKTDEVRIYMSHS-----LRYFLIIIPAVFGLSALSKPL 318
 QY 339 CFVWFVFNVSEKTLIDIGVDFAFALCVVPLRIFSPFVPTVRAHLTGWMLTKKTF 398
 Db 319 LGVLTQDFVSGWVFVPII---AFAGLVGIFQIF-----VNTFLIKKT- 360
 QY 399 VLAPSSVLRIIVLIA-----SLVPLVYLVGHGATLGVGSLLAGFVGBSTWVAIAACY 450
 Db 361 --RPATVINILAAVSNVLINLILIPSVGIAAGAL--STLVSYFLMAALCMRVTLKY 412
 RESULT 9
 ID Q8CNP2 PRELIMINARY; PRT; 511 AA.
 AC Q8CNP2
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE High affinity proline permease.
 GN SE1587.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016749; AAC05186.1; .
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001734; Na/solut_sympor.
 DR Pfam; PF00474; SSF; 1.
 DR TIGRFAMs; TIGR00813; sss; 1.
 DR PROSITE; PS0283; NA_SOLUT_SYMP_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 511 AA; 56025 MW; 2028D63BA046A568 CRC64;

Query Match 4.6%; Score 117.5; DB 16; Length 511;
 Best Local Similarity 19.7%; Pred. No. 0.18;
 Matches 93; Conservative 78; Mismatches 147; Indels 153; Gaps 22;
 QY 53 GLAYSIMKFFTPGMSDFKNVGLVFNVSKRDRTKAVLCMVVAGNAIAVFTLAYSDLGYI 112
 Db 117 GDAITLPDFKRLDDKNI-----IKISGLIIVVFPTL--YTHSGFV 158
 QY 113 IINKLHHVDESVGSKTRRAFVLAAPFPMDAMWTHAGILLKH-----KYSLVFG--CASI 166

Db 159 -----SGGK-----LFSAGFLN-----YHAGLLIVAIIVIFVTFGGYLA VSI 197
 Qy 167 SDVIAQVFAVAILHSHLECEPELIPILSLYMGALVRCCTLCGYGYNTHDIIPDR-SG 225
 Db 198 TDFQGVIMLIAM-----VNVPIVAL-----LKGWDTDFHDAQMKPTN 237
 Qy 226 PELGGDATIRKMLS-FWMLALILATORISRP-IVNLFS-----RDLGGSSAAT 273
 Db 238 LDLFRGTGTVLGIVSLFSGLGY-----FGQPHIIVRFMSIKSHKLLPKARRLG---ISW 288
 Qy 274 EAVAILTATYPVGHVPYCWLTB-----IRAVYPAPDKNPNKLVSTNTVTAHHIKKTF 329
 Db 289 MAVGLLGA-IGVLTGTSFISERHIKSDPDTLFI VMSQILFHPVLGVGFLAAILAAMS 347
 Qy 307 NPSKLVSTNTV-----AAHIKKTFFV---CMALSLLTLCFVMEWTFNVSE 350
 Db 348 TISSQLLVTSSTLDFYKLIRGSDKASHQKFEVLIGRLSVLLVAIVAITIAHPN--- 404
 Qy 351 KILDIIGVDFAPAEALCVVPIRISFFPVPVYVAHITGMLTKTFVLAPSVLRIV 410
 Db 405 DTILNLGVNAGFGAAPSPLVLSYWKDLTRAGASG-----MVAGAVV 450
 Qy 411 LIASLVLPYLGVGATGVGSLLAGFVGESTMVAIAACVYVRKOKKMN 461
 Db 451 VIVWISWKPLATINAFPGMYEILPGFI-----ISVLITIVSKLTKKPD 496

RESULT 10

Q9JTN5 PRELIMINARY; PRT; 693 AA.
 ID Q9JTN5
 AC Q9JTN5
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Putative integral membrane protein (CstA-like).
 GN NMA1698.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=656599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Mouls S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis 22491";
 RL Nature 404:502-506(2000).
 DR EMBL; AL162756; CAB84926.1; -
 DR PIR; E81865; E81865.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0009267; P:cellular response to starvation; IEA.
 DR InterPro; IPR003706; CstA.
 DR Pfam; PF02554; CstA; 1.
 KW Complete proteome.
 SQ SEQUENCE 693 AA; 74545 MW; 1FID706269C20B46 CRC64;

Query Match 4.6%; Score 117.5; DB 16; Length 693;
 Best Local Similarity 22.3%; Pred. No. 0.26;
 Matches 100; Conservative 63; Mismatches 149; Indels 137; Gaps 24;
 Qy 62 FTGPMDSFKNVGLVFPVNSKDRTRKAVLCWVAGAAVFTHTLIAYSDLYGVIINKLHVD 121
 Db 320 FSGALFFP-----LPI-----TIAGVSG-----FHALISGCTPKMLENETHVRM 361
 Qy 122 EVSGKTRAFVLYLAAPFMDAMANTHAGI-LLKHYSFLVGCASISDVIAQV----- 173
 Db 362 IGYGMLMESFVAIMA---LAAAALDPGVYFAMNSPAALIG--TDANTAETVITTKIQF 416

Qy 174 -VFVAILLHSHLECEPELIPILSLYMGALVRCCTLCGYGYNTHDIIPDRSGPGLGDA 232
 Db 417 PVDAATLHTAKEVEN---TILSPAGGA---PTLAVGMAHIMSRLLP-----GEA 461
 Qy 233 TIRKMLSFWMPLALIL-----ATORISRPVNLFVSRLDGG-----SSAAT 273
 Db 462 ----NMAFWYHPALLFEALFILTAVDAGTRVAR-----FMQDLGSIYFKPFGNTDSIPA 512
 Qy 274 EAVAILTATYPVGHVPYCWLTB-----IRAVYPAPDKNPNKLVSTNTVTAHHIKKTF 329
 Db 513 NLIATFFAVALMGYFLYTCGTDPLGGINSMLPF-----GIANQMLA----- 554
 Qy 330 VCMALSLLTLCFYMF-----WTPNVSEKILIDIIGVDFAPAEALCVVPIRISFFPVP 380
 Db 555 ---GVALINCVAVLIKMKRDRYVWV-----VLVPAVGVLV---TCYAGLQKLFHSDP 602
 Qy 381 VTVRAHLATGMLTKKTFVLAPS-----SVLRIT-----VLIAISVLPYLGVHGA 426
 Db 603 ISFLAHTGYSDALAKNEVLAPAKDIGEMAQIIFNDKINAGLTILFLSVVVI---VAAIGL 660
 Qy 427 TLGVGSLLAGFVGESTMVAIAACVYVRKQ 455
 Db 661 RT---ALKARKVGWPTAKEIPAVYEDGKQ 686

RESULT 11

Q8XT07 PRELIMINARY; PRT; 450 AA.
 ID Q8XT07
 AC Q8XT07
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Probable macrophage-efflux transmembrane protein.
 GN RSP0310 OR RS05460.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choigne N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646078; CAD17461.1; -
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000524; HTH GntR.
 DR InterPro; IPR007114; MFS.
 DR PROSITE; PS00043; HTH GNTX_FAMILY; 2.
 DR PROSITE; PS0850; MFS; 1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 450 AA; 46773 MW; 4F3715370BA4E5A6 CRC64;

Query Match 4.6%; Score 117; DB 16; Length 450;
 Best Local Similarity 20.8%; Pred. No. 0.17;
 Matches 100; Conservative 70; Mismatches 186; Indels 124; Gaps 19;
 Qy 29 FGEQALNRGIAAVKE-----DAVELASYGLAYSLMKFTGPMDSFKVGLVFPV 77
 Db 53 FGQALSLGSLTGTGVLWNITDTTGSVALATAGLALL-----POAVLSPUGTFA 106
 Qy 78 NSKRDTRKAVLCWVAGAAVFTHTLIAYSDLYGVIINK--LHHVDESVGSKTRAFVLY 135

Db 107 -----DRYSRRLMIVADGISALCMLLL-----IALFLTGRIALMHWAYVMMAIRS----- 151
Qy 136 AAFPNDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILLHSHLECREPILIPIL 195
Db 152 AAQAFAPAA--NASTVMLVPGFLVRAAGINOSLOSILV-----VAAPLG 196
Qy 196 SLVWGA-----VRCTTLCGYKXNHHIIPD-----RSGPELGSGATIRKMLSFWP-- 243
Db 197 ALAIGVMPICWALGIDVATALLGIAPLLCCRIPOACVSSGQKTGLMPAFREGVDLVWKT 256
Qy 244 -----LALILATORISRPINLVFVSRDLGSSAATEAVALLTATYPVGHMPVGLTE 295
Db 257 GLRWLVLCAGVLTIMPITLVLVLTWTFHFGAAA-----QVALMEGLSIGWVAGLL-- 311
Qy 296 IRVYPAFDKNPSNKLVSNTVNTAAHIKFTFVCMALSLLT-----CFVMPWTN 347
Db 312 VAAMAP-----RQVAVILCGFAMSCVALALTALAPGSLFGVAVAMVW-- 354
Qy 348 VSEKILLIIGVDFAPAEELCVPLRFSPFPVTVRAHLTGMLTKTKTFV-LAPSSVL 406
Db 355 -----ISGITVFVGNAPTAL-----LQTVNHLQGRVLSTLNTTGLAAPVGL 399
Qy 407 RIIVLASLVPLVPGVHGATLGVSLAGFVGESTWVAIAACVYVRKOKKMNESATE 466
Db 400 ALFTPLGEVIGVAFALFAIGLLGAASLAGFLSPSLM-----RLDRFSPSEARTD 450

RESULT 12

Q81F82 PRELIMINARY; PRT; 469 AA.
AC Q81F82; ID Q81F82
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE N4+ driven multidrug efflux pump.
GN BCI1716.
OS *Bacillus cereus* (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goleman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Fusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrides N.
RT "Genome sequence of *Bacillus cereus* and comparative analysis with
RT *Bacillus anthracis*."
RL Nature 423:87-91(2003).
DR EMBL; AE017003; AAF08692.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
KW Complete proteome.
SQ SEQUENCE 469 AA; 51613 MW; 1B831E84AE4231C CRC64;

Query Match 4.6%; Score 117; DB 16; Length 469;
Best Local Similarity 20.2%; Pred. No. 0.18;
Matches 98; Conservative 81; Mismatches 215; Indels 90; Gaps 20;

Qy 16 FLVPLGLTNTAID-----FGQALNRGIAA VKDAVEMLASVGLAYSLMKFFTGPMDFK- 70
Db 31 FLVPLLSNVLSVGLQFGVGVVGVWGLV--NDLAAISAFPLFLVSVFVIGSGSSI 88
Qy 71 NVGLVFNKRDRTKAVL-----CMVAGAAVFTHTLIAYSDLGYY-----IINKLHV 120
Db 89 LIGQAFGAKNEDRLKAVGTGTTFTFTFVIGVLLAIGSFAMINRLMGTPEINIEISVHY 148

Qy 121 DESVGSKTRAPFLYLAAPPFPMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
Db 149 ARILFISNPFVFLYFAVTTMRGTGDS-----KTPFVFLIVSTALN-----MILLPIL 197
Qy 181 HSHLECREPILIPILSLVWGA-----VRCTTLCGYKXNHHIIPD-RSGPELGSGATIRK- 236
Db 198 FGNLGA-----PKLDVYGAAYASVITVITFVYL--VYLKKNHPLQDGTVRKYLRLM 249
Qy 237 -----MLSFWMPLALILATORISRPINLVFVSRDLGSSAATEAVAILTATYPVGHMP 289
Db 250 DGEILLKULLRIGIPASINMILVLSLSEIAVAFVNR-YGSDATAAYGVVNVQVASV--QMP 306
Qy 290 YGWLTVRAVPAFDKNPSNKLVSNTVNTAAHIKFTFVCMALSLLTCLF-----VWFW 344
Db 307 AVSLGITVSIFAA--QSIGANQFDRLOKVKVAGIMNYVIGGVLLISLYVFSRDLSLFL 364
Qy 345 TPNVSEKILLIIGVD-----PFAELCVPLRFSPFPVTVRAHLTGMLTKTKTF 398
Db 355 TSQTTIEAHLVMTLSYLIFGHAQI-----ISATRASGT----- 402
Qy 399 VLAPSSVLRIIVLASLVPLVPGVHGATLGVSLAGFVGESTWVAIAACVYVRK--Q 455
Db 403 VLWPTVIGVWSIMLVEVFPVAYLTSYH-TSLGIEGIMIGYPA-AFIVSLILQYAYYKLSWQ 460
Qy 456 KKQM 459
Db 461 KKRI 464

RESULT 13

Q9RQ9 PRELIMINARY; PRT; 481 AA.
AC Q9RQ9; ID Q9RQ9
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Putative oligosaccharide repeat unit transporter.
GN CPS19CJ.
OS *Streptococcus pneumoniae*.
OC Bacteria; Firmicutes; Lactobacillales; *Streptococcaceae*;
OC *Streptococcus*.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99395043; PubMed=10464207;
RA Morona J.K., Morona R., Paton J.C.;
RA "Comparative genetics of capsular polysaccharide biosynthesis in
RT *Streptococcus pneumoniae* types belonging to serogroup 19."
RL J. Bacteriol. 181:5355-5364(1999).
DR EMBL; AF105116; AAD19923.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc synt.
DR Pfam; PF01943; Polysacc synt; 1.
SQ SEQUENCE 481 AA; 53798 MW; 4FECCCBF43CBBDAE CRC64;

Query Match 4.6%; Score 117; DB 2; Length 481;
Best Local Similarity 21.2%; Pred. No. 0.19;
Matches 102; Conservative 85; Mismatches 135; Indels 158; Gaps 30;

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Db 23 PPLIT--FPYISRLNPNGLTGFSSIG----NYGI-----LLASLGI----- 61
Qy 61 FFTGPMSPKFNKVLGVFNVSKEDRTKAVL--CMVAGAAVFTHTLIAYSDLGYYIINKLH 118
Db 62 -----SYGIKAVASVREDRDKLSKVQELMIINVASIITAILLFWTI---FITQLN 112
Qy 119 HVDESVGSKTRAPFLY-----AAPFDMAWTHAGILLKHYSFLVGCASISDVIA 171
Db 113 -----REFSLITCGTILSGPF--ALANWLYSGM--BEYTYITRSVVFILS 156
Qy 172 -----QVVFVAILLHSHLECREPILIPILSLVWGA----- 218


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Db 157 LILFLVLRPEDYVIFASISLSSN-----ILNLWHSR-----HFINI-- 198
Qy 219 IIPDRSGPLGDATIRKMLSF-----WWPLALILATORISRPVNLFSRD--LGGS 269
Db 199 -----KLYKNLOQKHFKPMWYLFASLLA-----VNIYTNLDTVMLG 236
Qy 270 SAATEAVAILPATYVGHMPYGMWTEIRAV-YPA-----FDKNPNPN--KLVSNTNTVTA 322
Db 237 INGEAVGYVSVASKVWILLSLITSISAVLLPRLSFYISKNDTSNFIKMKESSAV--- 293
Qy 323 HIKKFTFCMALSLTLCFWFWNTNVSSEKILIDIGVDFAFALC---VVPLRIFSPFPV 379
Db 294 -----IFFTAIPL-----WVFFIVEAKDSILL-LGGSQYLPATLAMQILMILLISGF-- 340
Qy 380 PVTVAHLTG-----WMLTKKTFVLAPSSVLRRIIVLIASLVVLYLGVHGATLGVGSLLA 435
Db 341 -----SNITGNQILIPMNRKYFMVA-VTIGAVINLIILMLPKFGIIGAS--VATLFA 392

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Q07870 ID C07870 PRELIMINARY; PRT; 481 AA.
AC C07870;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Putative oligosaccharide repeat unit transporter.
GN CPS19BU.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97386440; PubMed=9244289;
RA Morona J.K., Morona R., Paton J.C.;
RT "Molecular and genetic characterization of the capsule biosynthesis
RT locus of Streptococcus pneumoniae type 19B.";
RL J. Bacteriol. 179:4953-4958 (1997).
DR EMBL; AF004325; AAB66524.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; P:Polysacc_synt.
DR Pfam; PF01943; Polyseacc_synt; 1.
SQ SEQUENCE 481 AA; 53853 MW; C09A07D7D1AB5FD6 CRC64;

Query Match 4.6%; Score 117; DB 2; Length 481;
Best Local Similarity 21.0%; Pred. No. 0.19;
Matches 101; Conservative 85; Mismatches 136; Indels 158; Gaps 29;

Qy 4 FPALTYWPLI-RFLVP--LGINTAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMK 60
Db 23 FPLIT--FPYISRIILNPNGIGLTSFFSIG-----NYGI-----LLASLGI----- 61
Qy 61 FTGPMSPFNKVLGVFNVSKRDRKAVL--CMVAGATAAVPHTLIAYSDLYGIYINKLH 118
Db 62 -----STYGIKAVASVRDRDKLSKVQELMINVAMSIITTAIDLFMTI---FITQLN 112
Qy 119 HYDESVGSKTRAFYLL-----AAPPFMDAMWATHAGILLKKKYSFLVGCASISDVIA 171
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Qy 172 -----QVVFVAILHSHLECEPLIIPILSYMGALVRCCTLCGYKNIHD 218
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Qy 219 IIPDRSGPLGDATIRKMLSF-----WWPLALILATORISRPVNLFSRD--LGGS 269
Db 199 -----KLYKNLOQKHFKPMWYLFASLLA-----VNIYTNLDTVMLG 236
Qy 270 SAATEAVAILPATYVGHMPYGMWTEIRAV-YPA-----FDKNPNPN--KLVSNTNTVTA 322
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Qy 323 HIKKFTFCMALSLTLCFWFWNTNVSSEKILIDIGVDFAFALC---VVPLRIFSPFPV 379
Db 294 -----IFFTAIPL-----WVFFIVEAKDSILL-LGGSQYLPATLAMQILMILLISGF-- 340
Qy 380 PVTVAHLTG-----WMLTKKTFVLAPSSVLRRIIVLIASLVVLYLGVHGATLGVGSLLA 435
Db 341 -----SNITGNQILIPMNRKYFMVA-VTIGAVINLIILMLPKFGIIGAS--VATLFA 392

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Q07870 ID C07870 PRELIMINARY; PRT; 481 AA.
AC C07870;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Putative oligosaccharide repeat unit transporter.
GN CPS19BU.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97386440; PubMed=9244289;
RA Morona J.K., Morona R., Paton J.C.;
RT "Molecular and genetic characterization of the capsule biosynthesis
RT locus of Streptococcus pneumoniae type 19B.";
RL J. Bacteriol. 179:4953-4958 (1997).
DR EMBL; AF004325; AAB66524.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; P:Polysacc_synt.
DR Pfam; PF01943; Polyseacc_synt; 1.
SQ SEQUENCE 481 AA; 53853 MW; C09A07D7D1AB5FD6 CRC64;

Query Match 4.6%; Score 117; DB 2; Length 481;
Best Local Similarity 21.0%; Pred. No. 0.19;
Matches 101; Conservative 85; Mismatches 136; Indels 158; Gaps 29;

Qy 4 FPALTYWPLI-RFLVP--LGINTAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMK 60
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Qy 61 FTGPMSPFNKVLGVFNVSKRDRKAVL--CMVAGATAAVPHTLIAYSDLYGIYINKLH 118
Db 62 -----STYGIKAVASVRDRDKLSKVQELMINVAMSIITTAIDLFMTI---FITQLN 112
Qy 119 HYDESVGSKTRAFYLL-----AAPPFMDAMWATHAGILLKKKYSFLVGCASISDVIA 171
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Db 157 LILFLVLRPEDYVIFASISLSSN-----ILNLWHSR-----HFINI-- 198
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Db 199 -----KLYKNLOQKHFKPMWYLFASLLA-----VNIYTNLDTVMLG 236
Qy 270 SAATEAVAILPATYVGHMPYGMWTEIRAV-YPA-----FDKNPNPN--KLVSNTNTVTA 322
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DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
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DE 4F21c-5.
GN Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20473842; PubMed=10631289;
RA Rajan D.P., Kekuda R., Huang W., Devoe L.D., Leibach F.H.,
RA Prasad P.D., Ganapathy V.;
RT "Cloning and functional characterization of a Na(+)-independent,
RT broad-specific neutral amino acid transporter from mammalian
RT intestine.";
RL Biochim. Biophys. Acta 1463:6-14 (2000).
DR EMBL; AF170106; AAF26282.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015359; F:amino acid permease activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004760; L_AA_transporter.
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DR Pfam; PF00324; aa_permeases; 1.
DR TIGRFAMs; TIGR00911; 2A0308; 1.
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Qy 85 KAVLCMVAGATAAVPHTLIAYSDLYGIYINKLHHVDES VG--SKTRAFYLAAPPFMD 142
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Qy 282 TYP-----VGHMPYGMWTEIRAVYPAFDKNPNPNKLVST----- 316
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 17:21:47 ; Search time 1172 Seconds
(without alignments)
11329.272 Million cell updates/sec

Title: US-09-978-188A-6

Perfect score: 2945

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Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2945	100.0	2945	9	US-09-999-832A-6
5	2945	100.0	2945	10	US-09-978-189-6
6	2945	100.0	2945	10	US-09-978-609A-6
7	2945	100.0	2945	10	US-09-978-585A-6
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ALIGNMENTS

RESULT 1

US-09-978-295A-6
; Sequence 6, Application US/09978295A

; Patent No. US2002015606A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2945; DB 9; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGGTCAGCCACGCGGGGAGTATGTGAAATTCGCGGCGCTCACGCACTACTGGCCCT 120

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DB 121 GATCGGCTTCTTGGTGGCCCTCGGCGATCAACACATAGCCATCGATTCGGGGAGCAGG 180

QY 181 CTTGAACGGGGATTCGCTGTCAAGAGGATGAGTCGAGATGCTGGCAGACTACG 240
DB 181 CTTGAACGGGGATTCGCTGTCAAGAGGATGAGTCGAGATGCTGGCAGACTACG 240

QY 241 GCTGGCTACTCCCTCATGAAGTCTTCAAGGCTCCCATGAGTGAATTCAGAAATGTGG 300
DB 241 GCTGGCTACTCCCTCATGAAGTCTTCAAGGCTCCCATGAGTGAATTCAGAAATGTGG 300

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QY 481 GTACTCGCCCTTTCTTTTCAAGGAGCAATGGCATGGCATGGCATTTCTTT 540
DB 481 GTACTCGCCCTTTCTTTTCAAGGAGCAATGGCATGGCATGGCATTTCTTT 540

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DB 2521 TGCCAGGTTGCTGAGGTAACTTTTGAAGTGAATATATTTACCTGTTCTGCTATCCCTTA 2580
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DB 2581 GTCAATACTGCGGTACAGTAATTTGAGAACTGATGAGTCTTCCCTCCACACCAT 2640
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QY 2701 ACGATTCGAAATCCATGCGAGTGCAGTATATTTTCTAAAGTTTGAAGAGCGGTTTTTT 2760
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RESULT 3

US-09-978-188a-6

; Sequence 6, Application US/09978192A

; Patent No. US2002017553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey

; APPLICANT: Goddard, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 2945; DB 9; Length 2945;
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Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGACAGATGTGTG 60
DB 1 CGCTGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGACAGATGTGTG 60
QY 61 GGGTCAGCCACGCGGGGAGCTATGTTGAAATTCGCGCGCTCAGCAGTCTGCGCCCT 120
DB 61 GGGTCAGCCACGCGGGGAGCTATGTTGAAATTCGCGCGCTCAGCAGTCTGCGCCCT 120
QY 121 GATCCGGTCTTGGTGGCCCTGGGCATCACCAGATAGCATCGACTTCGGGAGCAGC 180
DB 121 GATCCGGTCTTGGTGGCCCTGGGCATCACCAGATAGCATCGACTTCGGGAGCAGC 180
QY 181 CTTGAACCGGGCATTTGCTGTCTCAAGGAGGATGAGTCAGATGCTGGCCAGCTACGG 240
DB 181 CTTGAACCGGGCATTTGCTGTCTCAAGGAGGATGAGTCAGATGCTGGCCAGCTACGG 240
QY 241 GCTGGGTACTCGCTCATGAAGTCTTTCACGGGTCCCATGAGTACTTCAAAATGTGGG 300
DB 241 GCTGGGTACTCGCTCATGAAGTCTTTCACGGGTCCCATGAGTACTTCAAAATGTGGG 300
QY 301 CTTGGTGTGTTGTAACAGCAGAGACAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGC 360
DB 301 CTTGGTGTGTTGTAACAGCAGAGACAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGC 360
QY 361 AGGGGCAATCGCTGCGCTTTTTCACACTGATAGTATAGTATAGTATAGTACTACTAT 420
DB 361 AGGGGCAATCGCTGCGCTTTTTCACACTGATAGTATAGTATAGTATAGTACTACTAT 420
QY 421 TATCAATAAATGCAACCATGTGGAGGTCGGTGGGAGCAAGACAGAGAGGCGCTTCTCT 480
DB 421 TATCAATAAATGCAACCATGTGGAGGTCGGTGGGAGCAAGACAGAGAGGCGCTTCTCT 480
QY 481 GTACCTCGCGCCCTTTTCCCTTTTCAAGCAGCAATGAGCATGAGCCATGCTGGCATCTCTT 540
DB 481 GTACCTCGCGCCCTTTTCCCTTTTCAAGCAGCAATGAGCATGAGCCATGCTGGCATCTCTT 540
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QY 541 AAAACACAAATACAGTTTCTGGTGGATGTGCTCAATCTCAGATGTCAATAGCTCAGGT 600
DB 541 AAAACACAAATACAGTTTCTGGTGGATGTGCTCAATCTCAGATGTCAATAGCTCAGGT 600
QY 601 TGTGTTTGTAGCCATTTGCTTGCATCAGTACCTGGAAATCGGGAGACCCCTGCTCATGCC 660
DB 601 TGTGTTTGTAGCCATTTGCTTGCATCAGTACCTGGAAATCGGGAGACCCCTGCTCATGCC 660
QY 661 GATCCCTCTCCCTGTATACATGGGCGCACTTGTGCGCTGCACACCCCTGTGCTGGGCTACTA 720
DB 661 GATCCCTCTCCCTGTATACATGGGCGCACTTGTGCGCTGCACACCCCTGTGCTGGGCTACTA 720
QY 721 CAAGAAATTCAGCAATCATCCCTGACAGAAATGSCCCGGAGCTGGGGGAGATGCAAC 780
DB 721 CAAGAAATTCAGCAATCATCCCTGACAGAAATGSCCCGGAGCTGGGGGAGATGCAAC 780
QY 781 AATAAGAAAGATGCTGAGCTTCTGCTGGCTTGGCTCTAATCTGGCCACACAGAGAAAT 840
DB 781 AATAAGAAAGATGCTGAGCTTCTGCTGGCTTGGCTCTAATCTGGCCACACAGAGAAAT 840
QY 841 CAGTCGGCTTATGTCAACCTCTTTGTTCCCGGACCTTGTGGGAGTTCTGCAAGCCAC 900
DB 841 CAGTCGGCTTATGTCAACCTCTTTGTTCCCGGACCTTGTGGGAGTTCTGCAAGCCAC 900
QY 901 AGAGGAGTGGGATTTGACAGCCACATACCTGTGGGTCAATGCCATACGGCTGGTT 960
DB 901 AGAGGAGTGGGATTTGACAGCCACATACCTGTGGGTCAATGCCATACGGCTGGTT 960
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QY 1021 GAGCAGGAGAAACACAGTACGAGCCACATCAAGAGTTTCACTTGTCTGCAATGAC 1080
DB 1021 GAGCAGGAGAAACACAGTACGAGCCACATCAAGAGTTTCACTTGTCTGCAATGAC 1080
QY 1081 TCTGTCACTCAGCTCTGTTTCTGATGTTTGGACACACCAGTGTCTGAGAAATCTT 1140
DB 1081 TCTGTCACTCAGCTCTGTTTCTGATGTTTGGACACACCAGTGTCTGAGAAATCTT 1140
QY 1141 GATAGACATCATCGAGTGAATTTGCTTGGAGAACTCTGTGTTGTTTCTTGGGAT 1200
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DB 1201 CTCTCTCTCTCCAGTCCAGTCAAGTGAAGGCGCATCTCACCGGTGGCTGATGAC 1260
QY 1261 ACTGAAGAAACCTTCTGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT 1320
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QY 1321 CAGCTCTGCTCTACCTTACCTTGGGGGTGACGCTGCGACCCCTGGGGTGGGCTCCCT 1380
DB 1321 CAGCTCTGCTCTACCTTACCTTGGGGGTGACGCTGCGACCCCTGGGGTGGGCTCCCT 1380
QY 1381 CTTGGCGGCTTTGTGGAGAAATCCACATGGTGGCCATCGCTGCGTGTATGCTACCG 1440
DB 1381 CTTGGCGGCTTTGTGGAGAAATCCACATGGTGGCCATCGCTGCGTGTATGCTACCG 1440
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DB 1441 GAACAGAAAGAGATGGAATGAGTGGCCACGAGGGGAGAGACTCTGCCATGAC 1500
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QY 1561 AGGACGGGACGCACTGGGCACTGACAGGACGCTCAGTCAAGATGACATTCGGGATCAT 1620
DB 1561 AGGACGGGACGCACTGGGCACTGACAGGACGCTCAGTCAAGATGACATTCGGGATCAT 1620
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DB 1681 GGCCTTGATTTAAAGGTTTGGTCAATTTCTAGCATATGCTAGCTAGCTAGCTAGCTAGCTAGCT 1740
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DB 1801 CATACCCCTGCTCAGCAAAACCCAAAGACACAGCTCCTCAGCTGCTGCTGCTGCTGCTGCTGCT 1860
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DB 2161 GACCTGTACACAGCAGGCTGACAGATGGAAGAAATCTCCCGTAGAAAGTTTGGTTG 2220
QY 2221 AAATGCCCCGGGGCAGCAACTGACATGTTGATGATAGCATTTCACTCTGCTGCTC 2280
DB 2221 AAATGCCCCGGGGCAGCAACTGACATGTTGATGATAGCATTTCACTCTGCTGCTC 2280
QY 2281 CTAGATCTGAGCAAGCTGTCACTGCTCTCACCCCCCGCTGTATATACATGAGCTAACTTTT 2340
DB 2281 CTAGATCTGAGCAAGCTGTCACTGCTCTCACCCCCCGCTGTATATACATGAGCTAACTTTT 2340
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DB 2521 TGCCAGGTTGCTGAGGGTAACTTTTGAAGTAGATATATACCTGGTCTGCTATCCCTTA 2580
QY 2581 GTCATAACTCTCGGTCAGGTAATTTAGTAATGTACTACGTACTTCCCTCCACACCAT 2640
DB 2581 GTCATAACTCTCGGTCAGGTAATTTAGTAATGTACTACGTACTTCCCTCCACACCAT 2640
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DB 2641 AGGTAAGGACGACATTTTATACGATACAGAGTCACTATGCTGCTCCTCCCTGAAATA 2700
QY 2701 AGGCAATTCGAAATCCATGAGTCACTATTTTCTAAAGTTTGGAAAGCAGGTTTCTT 2760

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Db 2701 ACGCATTCGAAATCCATGTCAGTCAGTATATTTTCTAAGTTTGGAAAGAGGTTTTT 2760
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
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; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
Qy 2821 AAGAACCTAAACAAAAAATATTTTAAAGATATATAAATATATGCTGTATATGTTATGTAAT 2880
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
Db 2821 AAGAACCTAAACAAAAAATATTTTAAAGATATATAAATATATGCTGTATATGTTATGTAAT 2880
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
Db 2941 AAAAA 2945
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR APPLICATION NUMBER: 60/082569
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; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/077649

RESULT 4
US-09-999-832A-6
; Sequence 6, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuc, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC83
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/082796
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; PRIOR APPLICATION NUMBER: 60/083336
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 2945; DB 9; Length 2945;
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Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GATCGGTTCTTGGTGCCCTCGGCGATCACCACATAGCCATGACCTTCGGGAGAGGC 180
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Db 361 AGGGGCAATCGCTGCCGTCTTTCACTATGATAGCTTATAGTGAATTTAGGATPACTAT 420
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Db 841 CAGTCGGCCTATTGTCACACCTCTTTGTTCCCGGAGCTTGGTGGAGTCTCAGCCAC 900
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Db 901 AGAGGAGTGGCGATTTTGACGCCACATACCTTGTGGTCACTGCTACATACGGCTGGT 960
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Db 1021 GAGCAGGCAACACAGTCAGCGAGCCCAACATCAAGAAGTTCACTTCGTCGATGGC 1080
QY 1081 TCTGTCACTACGCTCTGTTTCGTCGATGTTTGTGACACACCCAAACGTCGTGAGAAATCTT 1140
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Db 1561 AGGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
QY 1621 CTTCTCCTCCTCCCATGCTATTTTGTCCCTTTTGTCTTTTGTCTTTTGTCTTTT 1680
Db 1621 CTTCTCCTCCTCCCATGCTATTTTGTCCCTTTTGTCTTTTGTCTTTTGTCTTTT 1680
QY 1681 GGCCTTGATTTAAAGTTTCGTGCAATCTCTAGCATACCTGGGTATGCTCAGCTGACG 1740
Db 1681 GGCCTTGATTTAAAGTTTCGTGCAATCTCTAGCATACCTGGGTATGCTCAGCTGACG 1740
QY 1741 GGGGACCTAGTGAATGCTCTTTACTGTGCTATGTATGTAATAAACAACCACTGACTT 1800
Db 1741 GGGGACCTAGTGAATGCTCTTTACTGTGCTATGTATGTAATAAACAACCACTGACTT 1800
QY 1801 CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGGTTGAGCTGTGCTCC 1860
Db 1801 CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGGTTGAGCTGTGCTCC 1860
QY 1861 TCCTCCCTGAGCAATCTCCTCTTGGAAACCAAGAGCTGCTGCTGCTGCTGCTGCTG 1920
Db 1861 TCCTCCCTGAGCAATCTCCTCTTGGAAACCAAGAGCTGCTGCTGCTGCTGCTGCTG 1920
QY 1921 GTCACCTGCGACAGAGCGCCACAGACTCTCTGCTCCCTCTTCATGCTCTTTAAGATCAA 1980
Db 1921 GTCACCTGCGACAGAGCGCCACAGACTCTCTGCTCCCTCTTCATGCTCTTTAAGATCAA 1980
QY 1981 CAGGTTAAATCTCGGCTTCTTGAATGCTTCCAGTCACATGCGGTCAGAGAGATG 2040
Db 1981 CAGGTTAAATCTCGGCTTCTTGAATGCTTCCAGTCACATGCGGTCAGAGAGATG 2040
QY 2041 GAGCCCCGGTGGCTCTTAAATTTCCCTTCTGCAAGGAGTTCGAAACCATCTACTCCAC 2100
Db 2041 GAGCCCCGGTGGCTCTTAAATTTCCCTTCTGCAAGGAGTTCGAAACCATCTACTCCAC 2100

RESULT 5

US-09-978-189-6

; Sequence 6, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

QY 2101 ACATCAGAGCGGGTGGCAGCTGCGCCGGAGTCCCGTTCCACTGAGGAACGGA 2160
Db 2101 ACATCAGAGCGGGTGGCAGCTGCGCCGGAGTCCCGTTCCACTGAGGAACGGA 2160
QY 2161 GACCTGTGACCAACAGCAGCTGACAGATGAGCAATCTCCGTTAGAAAGTTTGGTTG 2220
Db 2161 GACCTGTGACCAACAGCAGCTGACAGATGAGCAATCTCCGTTAGAAAGTTTGGTTG 2220
QY 2221 AAATCCCGGGGCGAGCAATGACATGATGATGATGATGATGATGATGATGATGATGAT 2280
Db 2221 AAATCCCGGGGCGAGCAATGACATGATGATGATGATGATGATGATGATGATGATGAT 2280
QY 2281 CTAGATCTGAGCAAGCTGTGCTGCTTCCACCCCGCCAGCTGATATATACATGAGCAATCTTT 2340
Db 2281 CTAGATCTGAGCAAGCTGTGCTGCTTCCACCCCGCCAGCTGATATATACATGAGCAATCTTT 2340
QY 2341 TTAATTTGTCACAAAGCGCATCTCCAGATTCAGACCTCCGCGATGACATCTTCTGAA 2400
Db 2341 TTAATTTGTCACAAAGCGCATCTCCAGATTCAGACCTCCGCGATGACATCTTCTGAA 2400
QY 2401 GGCCTTGCCTTCCCTCGCTTCTTCTGAAAGGTCGCAATAGAGCGAGTCAATGGAGCATCC 2460
Db 2401 GGCCTTGCCTTCCCTCGCTTCTTCTGAAAGGTCGCAATAGAGCGAGTCAATGGAGCATCC 2460
QY 2461 TTAATTTGCAATTTAGTTTTCAGTGAACTGAAAGCTTTAAGTCTCATCCAGCATCTAA 2520
Db 2461 TTAATTTGCAATTTAGTTTTCAGTGAACTGAAAGCTTTAAGTCTCATCCAGCATCTAA 2520
QY 2521 TGCAGGTTGCTGTAGGGTAACTTTTGAAGTAGATATATACCTGGTCTGTATCTCTTA 2580
Db 2521 TGCAGGTTGCTGTAGGGTAACTTTTGAAGTAGATATATACCTGGTCTGTATCTCTTA 2580
QY 2581 GTCATAACTCTCGGTCAGGTAATGAGATGTAAGTACTACGGTACTTCCCTCCCAACCAT 2640
Db 2581 GTCATAACTCTCGGTCAGGTAATGAGATGTAAGTACTACGGTACTTCCCTCCCAACCAT 2640
QY 2641 AGGATAAAGCAAGACATTTTATAAGATACAGAGTCACTATGCTGCTCCTCCGAAATA 2700
Db 2641 AGGATAAAGCAAGACATTTTATAAGATACAGAGTCACTATGCTGCTCCTCCGAAATA 2700
QY 2701 AGCATTCGAAATCCATGCGAGTCACTATTTTCTAAGTTTGGAAAGCAGGTTTTTT 2760
Db 2701 AGCATTCGAAATCCATGCGAGTCACTATTTTCTAAGTTTGGAAAGCAGGTTTTTT 2760
QY 2761 CTTTTTAAAAAATATAGCAGGTTCACTAAATGATTTAGTCAAGATTCCTAGACTGA 2820
Db 2761 CTTTTTAAAAAATATAGCAGGTTCACTAAATGATTTAGTCAAGATTCCTAGACTGA 2820
QY 2821 AAGAACCTTAAACAAAAAATATTTTAAAGATATAAATATATGCTGATATGTTATGTAAT 2880
Db 2821 AAGAACCTTAAACAAAAAATATTTTAAAGATATAAATATATGCTGATATGTTATGTAAT 2880
QY 2881 TTAATTTAGGCTTAATACATTTCTTATTTTCCGATTTTCAATTAATGCTCTTAATACA 2940
Db 2881 TTAATTTAGGCTTAATACATTTCTTATTTTCCGATTTTCAATTAATGCTCTTAATACA 2940
QY 2941 AAAAA 2945
Db 2941 AAAAA 2945

RESULT 5

US-09-978-189-6

; Sequence 6, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/085311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
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PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-27
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29

[illegible]

; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-978-608A-6									
Query Match 100.0%; Score 2945; DB 10; Length 2945;									
Best Local Similarity 100.0%; Pred. No 0;									
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CGCTCGCCCGCTGCCCTCCCGCAGAGTCCCTCGCGGACAGAGTGTGTG	60						
Db	1	CGCTCGCCCGCTGCCCTCCCGCAGAGTCCCTCGCGGACAGAGTGTGTG	60						
Qy	61	GGGTACGCCACGCGGGGACTGTGTAATCCCGCGCTCAGCACTACTGCGCCCT	120						
Db	61	GGGTACGCCACGCGGGGACTGTGTAATCCCGCGCTCAGCACTACTGCGCCCT	120						
Qy	121	GATCGGTTCTTGTGTGCCCTGGGCATCACCACATAGCCATCGACTTCGGGGAGCAGC	180						
Db	121	GATCGGTTCTTGTGTGCCCTGGGCATCACCACATAGCCATCGACTTCGGGGAGCAGC	180						
Qy	181	CTTGAAACCGGGCATTTGCTGTCAAGGAGTGCAGTGCAGATGCTGGCCACTACGG	240						
Db	181	CTTGAAACCGGGCATTTGCTGTCAAGGAGTGCAGTGCAGATGCTGGCCACTACGG	240						
Qy	241	GCTGCGTACTCCCTCATGAAGTCTTCAACGGTCCCATGAGTCACTTCAAAAATGTGG	300						
Db	241	GCTGCGTACTCCCTCATGAAGTCTTCAACGGTCCCATGAGTCACTTCAAAAATGTGG	300						
Qy	301	CCTGTGTTTGTGAACAGACAGAGACAGACCAAGCCGTCTGTGTATGTGTGTGGC	360						
Db	301	CCTGTGTTTGTGAACAGACAGAGACAGACCAAGCCGTCTGTGTATGTGTGTGGC	360						
Qy	361	AGGGCCCATCGTGCCTCTTTCACACTGATAGCTTATAGTATATAGATACTACAT	420						
Db	361	AGGGCCCATCGTGCCTCTTTCACACTGATAGCTTATAGTATATAGATACTACAT	420						
Qy	421	TATCAATAAATGCAACATGTGGAGTCTGGTGGGGAGCAAGACGAGAGGGCCTTCCT	480						
Db	421	TATCAATAAATGCAACATGTGGAGTCTGGTGGGGAGCAAGACGAGAGGGCCTTCCT	480						
Qy	481	GTACCTCGCGCTTCTTTCATGGACGCAATGGCATGGACCATGCTGCATCTCTT	540						
Db	481	GTACCTCGCGCTTCTTTCATGGACGCAATGGCATGGACCATGCTGCATCTCTT	540						
Qy	541	AAAAACAATAACAGTTTCTGGTGGGATGTGCTCAATCTCAGATGTATAGTCAAGT	600						
Db	541	AAAAACAATAACAGTTTCTGGTGGGATGTGCTCAATCTCAGATGTATAGTCAAGT	600						
Qy	601	TGTTTTGTAGCATTTTCTTCAGTCAGTCAGTGAATGCCGGAGCCCTGCTCATCCC	660						
Db	601	TGTTTTGTAGCATTTTCTTCAGTCAGTCAGTGAATGCCGGAGCCCTGCTCATCCC	660						
Qy	661	GATCCTCTCTTGTACATGGGCGACTTGTGGCTGACACCCCTGTGCTGGGCTACTA	720						
Db	661	GATCCTCTCTTGTACATGGGCGACTTGTGGCTGACACCCCTGTGCTGGGCTACTA	720						
Qy	721	CAAGAACATTCAGACATATCCCTGACAGAGTGGCGGAGTGGGGGAGATGCAAC	780						
Db	721	CAAGAACATTCAGACATATCCCTGACAGAGTGGCGGAGTGGGGGAGATGCAAC	780						
Qy	781	AATAAGAAAGATGCTGAGCTTCTGTGGCTTTGGCTCTAATCTTGGGCCACACAGAGAT	840						
Db	781	AATAAGAAAGATGCTGAGCTTCTGTGGCTTTGGCTCTAATCTTGGGCCACACAGAGAT	840						
Qy	841	CAGTCGGCTATGTCAACCTCTTGTTCGGGACCTTGGTGCAGTCTTGCAGCCAC	900						
Db	841	CAGTCGGCTATGTCAACCTCTTGTTCGGGACCTTGGTGCAGTCTTGCAGCCAC	900						
Qy	901	AGAGGAGTGGGATTTTACAGCCACATACCTCTGTGGTCAATGCCATACGGCTGGT	960						
Db	901	AGAGGAGTGGGATTTTACAGCCACATACCTCTGTGGTCAATGCCATACGGCTGGT	960						
Qy	961	GACGAAATCCGTGTGTGTATCTCTGCTTTTCAGAGAAATATACCCACGACAAACTGGT	1020						
Db	961	GACGAAATCCGTGTGTGTATCTCTGCTTTTCAGAGAAATATACCCACGACAAACTGGT	1020						

Db 2041 GAGCCCCGGTGGCCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCAC 2100
Qy 2101 ACATCAGAGCGGGTGGCGAGTCCCGGAGTCCCGGTTTACACTGAGGAACGGA 2160
Db 2101 ACATCAGAGCGGGTGGCGAGTCCCGGAGTCCCGGTTTACACTGAGGAACGGA 2160
Qy 2161 GACCTGTACACAGCAGCGGTGACAGATGAGAGTCCCGGTAGAAAGTTGGTTG 2220
Db 2161 GACCTGTACACAGCAGCGGTGACAGATGAGAGTCCCGGTAGAAAGTTGGTTG 2220
Qy 2221 AAATGCCCGGGGAGAGAACTGACATGTTGAATGATAGATTTCACTCTCGGTTCTC 2280
Db 2221 AAATGCCCGGGGAGAGAACTGACATGTTGAATGATAGATTTCACTCTCGGTTCTC 2280
Qy 2281 CTAGATCTGAGCAAGCTGTCACTTCTACCCGCCACCGGTGATATACATGAGCTAACTTTT 2340
Db 2281 CTAGATCTGAGCAAGCTGTCACTTCTACCCGCCACCGGTGATATACATGAGCTAACTTTT 2340
Qy 2341 TTAATATTGTCACAAAGCGCATCTCCAGATTCACAGCTCCGCGATGACTTTTCTGAA 2400
Db 2341 TTAATATTGTCACAAAGCGCATCTCCAGATTCACAGCTCCGCGATGACTTTTCTGAA 2400
Qy 2401 GGCCTTGCTTTCCCTCGCCCTTTCTGAAGTTCGCATTTAGAGCGAGTCAATGAGCATCC 2460
Db 2401 GGCCTTGCTTTCCCTCGCCCTTTCTGAAGTTCGCATTTAGAGCGAGTCAATGAGCATCC 2460
Qy 2461 TTAACCTTGATTTAGTTTACAGTAAGTTCAGGCTTTAAGTCTCATCCAGCTTCTAA 2520
Db 2461 TTAACCTTGATTTAGTTTACAGTAAGTTCAGGCTTTAAGTCTCATCCAGCTTCTAA 2520
Qy 2521 TGCAGGTTGCTGTAGGGTAACTTTTGAAGTAGATATATTACCTGGTTCTGTATCTCTTA 2580
Db 2521 TGCAGGTTGCTGTAGGGTAACTTTTGAAGTAGATATATTACCTGGTTCTGTATCTCTTA 2580
Qy 2581 GTCATTAACCTGCGGTACAGGTAATTTGAGATTTGAGATTTGAGTACTTCCCTCCACACCAT 2640
Db 2581 GTCATTAACCTGCGGTACAGGTAATTTGAGATTTGAGATTTGAGTACTTCCCTCCACACCAT 2640
Qy 2641 ACGATAAGCAAGACATTTTATAACGATACAGAGTCACTATGTGCTCCCTCGAAATA 2700
Db 2641 ACGATAAGCAAGACATTTTATAACGATACAGAGTCACTATGTGCTCCCTCGAAATA 2700
Qy 2701 ACGCATTGCAAAATCCATGACAGTGCAGTATTTTCTAAGTTTGGAAAGCAGGTTTTT 2760
Db 2701 ACGCATTGCAAAATCCATGACAGTGCAGTATTTTCTAAGTTTGGAAAGCAGGTTTTT 2760
Qy 2761 CTTTAAATAAATATAGACACGGTTTCACTAATTTAGTTCAGATTTAGTTCAGATTTAGTAA 2820
Db 2761 CTTTAAATAAATATAGACACGGTTTCACTAATTTAGTTCAGATTTAGTTCAGATTTAGTAA 2820
Qy 2821 AAGAACCCTAAACAAATAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAAT 2880
Db 2821 AAGAACCTAAACAAATAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAAT 2880
Qy 2881 TTATTTAGGCTAATATACATTTCTCTATTTTCGATTTTCAATTAATGTCCTATATA 2940
Db 2881 TTATTTAGGCTAATATACATTTCTCTATTTTCGATTTTCAATTAATGTCCTATATA 2940
Qy 2941 AAAAA 2945
Db 2941 AAAAA 2945

RESULT 7
US-09-978-585A-6
; Sequence 6, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: ROY, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 6
LENGTH: 2945
TYPE: DNA
ORGANISM: Homo sapiens
US-09-978-585A-6
Query Match 100.0%; Score 2945; DB 10; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCTCGCCCGTCCCGCCCTCCCGCCGAGAGTCCCTCGCGGACGAGATGTGTGTG 60
Db 1 CGCTCGCCCGTCCCGCCCTCCCGCCGAGAGTCCCTCGCGGACGAGATGTGTGTG 60
Qy 61 GGGTCAGCCACGCGGGGACATATGTGAAATCCCGGCGCTCAGCAGTACTTGGCCCCCT 120
Db 61 GGGTCAGCCACGCGGGGACATATGTGAAATCCCGGCGCTCAGCAGTACTTGGCCCCCT 120
Qy 121 GATCGGTTCTTGTGCGCCCTCGGCATCACCACATAGCCATCGACTTCGGGGAGCAGGC 180
Db 121 GATCGGTTCTTGTGCGCCCTCGGCATCACCACATAGCCATCGACTTCGGGGAGCAGGC 180
Qy 181 CTTGAACCGGGCATTTGCTGTCTCAAGGAGGATGAGTGTGCGGAGTGTGGCCAGCTACGG 240
Db 181 CTTGAACCGGGCATTTGCTGTCTCAAGGAGGATGAGTGTGCGGAGTGTGGCCAGCTACGG 240
Qy 241 GCTGCGTACTCCCTCATGAGTTCTTTCAGCGGTCCTCATGAGTGTGACATTTCAAAATGTGGG 300
Db 241 GCTGCGTACTCCCTCATGAGTTCTTTCAGCGGTCCTCATGAGTGTGACATTTCAAAATGTGGG 300
Qy 301 CCTGTGTTGTGAACAGCAAGAGAGCAGACCAAGCCCTCCTGTGTATGTGTGGTGGC 360
Db 301 CCTGTGTTGTGAACAGCAAGAGAGCAGACCAAGCCCTCCTGTGTATGTGTGGTGGC 360
Qy 361 AGGGCCATCGCTGCGGCTTTTCACACTGATAGCTTATAGTATTTAGGATATACAT 420
Db 361 AGGGCCATCGCTGCGGCTTTTCACACTGATAGCTTATAGTATTTAGGATATACAT 420
Qy 421 TATCAATAAATCTGCACCATTTGGAGCGAGTCCGGTGGGAGCAAGACGAGAGGGCTTCT 480
Db 421 TATCAATAAATCTGCACCATTTGGAGCGAGTCCGGTGGGAGCAAGACGAGAGGGCTTCT 480
Qy 481 GTACCTCGCCGCTTCTTCTTCATGAGCAATGCGATGCGACCCCATGCTGCGCATTTCTCT 540

QY 2701 ACGCATTCGAAATCCATGCGAGTGCAGTATATATTTTCTAAGTTTTCGAAAGCAGGTTTTT 2760
Db 2701 ACGCATTCGAAATCCATGCGAGTGCAGTATATATTTTCTAAGTTTTCGAAAGCAGGTTTTT 2760
QY 2761 CTTTAAATAAATATAGACACGGTTTCACTAAATGATTAGTTCAGAAATTCCTAGACTGA 2820
Db 2761 CTTTAAATAAATATAGACACGGTTTCACTAAATGATTAGTTCAGAAATTCCTAGACTGA 2820
QY 2821 AAGAACCTAAACAAAAAATATTTTAAAGATATAAATATATCTGTATATGTATGTAA 2880
Db 2821 AAGAACCTAAACAAAAAATATTTTAAAGATATAAATATATCTGTATATGTATGTAA 2880
QY 2881 TTATTTAGCTATATATACATTTCCCTATTTTCGCAATTTTCAATAAATCTCTCTAATACA 2940
Db 2881 TTATTTAGCTATATATACATTTCCCTATTTTCGCAATTTTCAATAAATCTCTCTAATACA 2940
QY 2941 AAAAA 2945
Db 2941 AAAAA 2945

RESULT 8

US-09-978-191A-6
; Sequence 6, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830FIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2945; DB 10; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGCTCGCCCGTGGCCCTCGCTCGCCGAGAGTCCCTCGCGCAGACAGATGTGTG 60
Qy 61 GGGTCAGCCACCGGGGGGCACTATGTTGAAATTCGCCGGCTCAGCGACTACTGCCCT 120
Db 61 GGGTCAGCCACCGGGGGGCACTATGTTGAAATTCGCCGGCTCAGCGACTACTGCCCT 120
Qy 121 GATCCGGTTCCTGGTGGCCCTCGCTCGCCGATACCAACATAGCCATTCGCGGAGCAGGC 180
Db 121 GATCCGGTTCCTGGTGGCCCTCGCTCGCCGATACCAACATAGCCATTCGCGGAGCAGGC 180
Qy 181 CTTGAACCGGGGCACTGCTGCTCAAGGAGATCAGTCGAGATGCTGGCCAGTACGG 240
Db 181 CTTGAACCGGGGCACTGCTGCTCAAGGAGATCAGTCGAGATGCTGGCCAGTACGG 240
Qy 241 GCTGGGTACTCCCTCATGAAGTCTTCAAGGATCCCATGAGTGAATTCAGAAATGTGG 300
Db 241 GCTGGGTACTCCCTCATGAAGTCTTCAAGGATCCCATGAGTGAATTCAGAAATGTGG 300
Qy 301 CTTGGTGTGTTGTAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 CTTGGTGTGTTGTAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 AGGGGCAATCGTGGCTCTTTCACACATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 AGGGGCAATCGTGGCTCTTTCACACATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 TATCAATAACTGACCATGTCGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 TATCAATAACTGACCATGTCGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 GTACCTCGCCGCTTTCCTTTCATGAGCAGATGAGCAGATGAGCAGATGAGCAGAT 540
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Qy 541 AAAACACAAATACAGTTTCCTGGTGGATGTCCTCAATCTCAGATGTCATAGTCAGGT 600
Db 541 AAAACACAAATACAGTTTCCTGGTGGATGTCCTCAATCTCAGATGTCATAGTCAGGT 600
Qy 601 TGTGTTGTAGCCATTTTCCTTTCATGAGCAGATGAGCAGATGAGCAGATGAGCAGAT 660
Db 601 TGTGTTGTAGCCATTTTCCTTTCATGAGCAGATGAGCAGATGAGCAGATGAGCAGAT 660
Qy 661 GATCCTCTCTGTATACATGGGCGCACTTGTGGCTGACACACCTGTGCTGGGCTACTA 720
Db 661 GATCCTCTCTGTATACATGGGCGCACTTGTGGCTGACACACCTGTGCTGGGCTACTA 720
Qy 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCCGGAGCTGGGGGAGATGCAAC 780
Db 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCCGGAGCTGGGGGAGATGCAAC 780
Qy 781 AATAAGAAAGATGTCAGCTTCTGGTGGCTTCTAAATTCGAGCAGACAGAGAGAT 840
Db 781 AATAAGAAAGATGTCAGCTTCTGGTGGCTTCTAAATTCGAGCAGACAGAGAGAT 840
Qy 841 CAGTCGGCTATTGTCAACCTCTTTTCCCGGAGACCTTGGTGGCAGTTCTGAGCCAC 900
Db 841 CAGTCGGCTATTGTCAACCTCTTTTCCCGGAGACCTTGGTGGCAGTTCTGAGCCAC 900
Qy 901 AGAGGAGTGGGATTTTTCAGAGCAGACATACCTGTGGTGCATGATGATGATGATGAT 960
Db 901 AGAGGAGTGGGATTTTTCAGAGCAGACATACCTGTGGTGCATGATGATGATGATGAT 960

QY	961	GACGAAATCCGTGTCGTGTATCTCTTTCGACAAAGAAATAACCCAGCAACAACTGGT	1020
DB	961	GACGAAATCCGTGTCGTGTATCTCTTTCGACAAAGAAATAACCCAGCAACAACTGGT	1020
QY	1021	GAGCAGGACACACAGTACAGGCAGCCACATCAAGAAGTTTCACCTTCGTCTGCATGGC	1080
DB	1021	GAGCAGGACACACAGTACAGGCAGCCACATCAAGAAGTTTCACCTTCGTCTGCATGGC	1080
QY	1081	TCGTCACTACGCTCTGTTTCGTGATGTTTGGACACCCACGFGTCTGAGAAAATCTT	1140
DB	1081	TCGTCACTACGCTCTGTTTCGTGATGTTTGGACACCCACGFGTCTGAGAAAATCTT	1140
QY	1141	GATAGACATCATCGAGTGGACTTTGCTTCGACGAATCTGTGTGTCTTTCGCGAT	1200
DB	1141	GATAGACATCATCGAGTGGACTTTGCTTCGACGAATCTGTGTGTCTTTCGCGAT	1200
QY	1201	CTTCTCCTTCTCCAGTTCACAGTGAAGGCGCATCTCACCGGGTGCGTATGAC	1260
DB	1201	CTTCTCCTTCTCCAGTTCACAGTGAAGGCGCATCTCACCGGGTGCGTATGAC	1260
QY	1261	ACTGAAGAAAACTTTCGTCTTTCGCCCCAGCTCTGTGCTGCGGATCATGCTCATCGC	1320
DB	1261	ACTGAAGAAAACTTTCGTCTTTCGCCCCAGCTCTGTGCTGCGGATCATGCTCATCGC	1320
QY	1321	CAGCCTCGTGGTCTTACCCTACCTCGCGGGTGACAGGTGCGACCCCTGGCGTGGCTCCCT	1380
DB	1321	CAGCCTCGTGGTCTTACCCTACCTCGCGGGTGACAGGTGCGACCCCTGGCGTGGCTCCCT	1380
QY	1381	CTTGGCGGGCTTTGTGGAGAAATCCACATGTCGCCATCGCTGCGTGTATGCTACGG	1440
DB	1381	CTTGGCGGGCTTTGTGGAGAAATCCACATGTCGCCATCGCTGCGTGTATGCTACGG	1440
QY	1441	GAGCAGAAAAAGAAATGAGAAATCAGTCGGGCCACGGAGGGGGAAGACTCTGCCATGAC	1500
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QY	1501	AGACATGCTCCGACAGAGAGGTGACAGACATCTGTGGAAATGAGAGAGAGAAATGAATA	1560
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QY	1561	AGCAGCGGAGCCATGGCAGCTCGAGGACGGTCAGTCAGGATGACACTTCGGCATCAT	1620
DB	1561	AGCAGCGGAGCCATGGCAGCTCGAGGACGGTCAGTCAGGATGACACTTCGGCATCAT	1620
QY	1621	CTCTTCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTTCCTTTTTTGGTAAGAAAGA	1680
DB	1621	CTCTTCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTTCCTTTTTTGGTAAGAAAGA	1680
QY	1681	GGCCTTGATTTAAAGTTTCGTGTCAATCTCTAGCATCTCGGGTATGCTCACACATGACG	1740
DB	1681	GGCCTTGATTTAAAGTTTCGTGTCAATCTCTAGCATCTCGGGTATGCTCACACATGACG	1740
QY	1741	GGGGGACCTAGTGAATGCTTTACTGTCTGCTATGTATAAAACAAACGAAACAACTGACTT	1800
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QY	1801	CATACCTTGCTCACGAAAAACCAAAAGACACAGCTGCCTCACGGTTGAGCTTGTGTCC	1860
DB	1801	CATACCTTGCTCACGAAAAACCAAAAGACACAGCTGCCTCACGGTTGAGCTTGTGTCC	1860
QY	1861	TCCTCCCTGGACAAATCTCTCTTGGAAACCAAAAGACTGACGCTGTGCCATCGCGCTCG	1920
DB	1861	TCCTCCCTGGACAAATCTCTCTTGGAAACCAAAAGACTGACGCTGTGCCATCGCGCTCG	1920
QY	1921	GTACCTCTGCACAGAGGCCACAGACTCTCTGTGCTCCCTTCATCGCTCTTAGAATCAA	1980
DB	1921	GTACCTCTGCACAGAGGCCACAGACTCTCTGTGCTCCCTTCATCGCTCTTAGAATCAA	1980
QY	1981	CAGGTTAAACCTCGGCTTCTTGATTTGCTTCCAGTCAATCGCCGTTACAAAGAGATG	2040
DB	1981	CAGGTTAAACCTCGGCTTCTTGATTTGCTTCCAGTCAATCGCCGTTACAAAGAGATG	2040
QY	2041	GAGCCCGGTCGCTCTTAAATTTTCCCTCTGCCCAGCGAGTTGAAACCACTTACTCCAC	2100

RESULT 9
US-09-978-403A-6
Sequence 6, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29

[illegible]

D _b	1381	CCTGGCGGCGCTTTGTGGGAGAAATCCACCATTGTCGCCCATCGCTGCCTGCTATGCTACCG	1440
Q _y	1441	GAAGCAGAAAAAAGAAGATGGAGAAATGAGTCGGCCACGGAGGGGGAAGACTCTGCCATCAC	1500
D _b	1441	GAAGCAGAAAAAAGAAGATGGAGAAATGAGTCGGCCACGGAGGGGGAAGACTCTGCCATCAC	1500
Q _y	1501	AGACATGCCCTCCGACAGAGAGGAGTGCACACATCGTGGAAAATGAGAGAGGAGAAATGAATA	1560
D _b	1501	AGACATGCCCTCCGACAGAGAGGAGTGCACACATCGTGGAAAATGAGAGAGGAGAAATGAATA	1560
Q _y	1561	AGGCACGGGACGCCATGGGCACTGCAGGAGCGGTCACTCAGGATGACACATTCGGGATCAT	1620
D _b	1561	AGGCACGGGACGCCATGGGCACTGCAGGAGCGGTCACTCAGGATGACACATTCGGGATCAT	1620
Q _y	1621	CTCTCCCTCTCCCATCGTAAATTTTGTTTCCTTTTTTTTGTGTTTGTGTTTGGTAATCAAAGA	1680
D _b	1621	CTCTCCCTCTCCCATCGTAAATTTTGTTTCCTTTTTTTTGTGTTTGTGTTTGGTAATCAAAGA	1680
Q _y	1681	GGCCTTGATTTAAAGGTTTCGTGTCAAATTCCTCPAGCATACTGGGTATGTCACACTGAGG	1740
D _b	1681	GGCCTTGATTTAAAGGTTTCGTGTCAAATTCCTCPAGCATACTGGGTATGTCACACTGAGG	1740
Q _y	1741	GGGGGACCTAGTCAATGGTCTTTTACTGTGGTATGTAAAAACAACAAACAACTGACTT	1800
D _b	1741	GGGGGACCTAGTCAATGGTCTTTTACTGTGGTATGTAAAAACAACAAACAACTGACTT	1800
Q _y	1801	CATACCCCTGGCTCACGAAAAACCAAAAGACACAGCTGCTCACGGTTGACGTTGTGTCC	1860
D _b	1801	CATACCCCTGGCTCACGAAAAACCAAAAGACACAGCTGCTCACGGTTGACGTTGTGTCC	1860
Q _y	1861	TCTCCTCCCTGGACAAATCTCCTCTTTGGAAAACAAAGGACTGCAGCTGTGCCATCGCGCTCG	1920
D _b	1861	TCTCCTCCCTGGACAAATCTCCTCTTTGGAAAACAAAGGACTGCAGCTGTGCCATCGCGCTCG	1920
Q _y	1921	GTCACCTGCACAGCAGGCGCACAGCTCTCTGTGCGCCTTATCGCTCTTAAGATCAA	1980
D _b	1921	GTCACCTGCACAGCAGGCGCACAGCTCTCTGTGCGCCTTATCGCTCTTAAGATCAA	1980
Q _y	1981	CAGGTTAAAAACTCGGCTTCTTTGATTTGCTTCCCAGTCAACATGGCCGTACAAAGAGATG	2040
D _b	1981	CAGGTTAAAAACTCGGCTTCTTTGATTTGCTTCCCAGTCAACATGGCCGTACAAAGAGATG	2040
Q _y	2041	GAGCCCCGGTGGCTCTTTAAATTTCCCTTCTGCAAGGAGTTGGAACCATCTACTCCAC	2100
D _b	2041	GAGCCCCGGTGGCTCTTTAAATTTCCCTTCTGCAAGGAGTTGGAACCATCTACTCCAC	2100
Q _y	2101	ACATGCAGGAGGGGGTGGCAAGCTGCAGCCCCGGAGTCCCGTTCACTCTGAGAACGGA	2160
D _b	2101	ACATGCAGGAGGGGGTGGCAAGCTGCAGCCCCGGAGTCCCGTTCACTCTGAGAACGGA	2160
Q _y	2161	GACCTGTGACACAGCAGGCTGACAGATGACAGATCTCCCGTAGAAAGTTTGGTTTG	2220
D _b	2161	GACCTGTGACACAGCAGGCTGACAGATGACAGATCTCCCGTAGAAAGTTTGGTTTG	2220
Q _y	2221	AAATGCCCCCGGGGACACAACTGACATGGTTGAAATGATAGCATTTCACTCTCGTTCTC	2280
D _b	2221	AAATGCCCCCGGGGACACAACTGACATGGTTGAAATGATAGCATTTCACTCTCGTTCTC	2280
Q _y	2281	CTAGATCTGAGCAAGCTGTCAAGTTCTCACCCCCACCGGTGATATACATGAGCTTAACTTTT	2340
D _b	2281	CTAGATCTGAGCAAGCTGTCAAGTTCTCACCCCCACCGGTGATATACATGAGCTTAACTTTT	2340
Q _y	2341	TTAAATTTGTCAAAAAGCGCATCTCCAGATTCAGACCCCTCGCGCATGACTTTTCTGTAA	2400
D _b	2341	TTAAATTTGTCAAAAAGCGCATCTCCAGATTCAGACCCCTCGCGCATGACTTTTCTGTAA	2400
Q _y	2401	GGCTTGCTTTTCCCTCGCCTTCTCTGAGGTCGCAATTAGAGCGGATCACATGAGGATCC	2460
D _b	2401	GGCTTGCTTTTCCCTCGCCTTCTCTGAGGTCGCAATTAGAGCGGATCACATGAGGATCC	2460
Q _y	2461	TAACTTTTGCAATTTTAGTTTTTACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATCTAA	2520
D _b	2461	TAACTTTTGCAATTTTAGTTTTTACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATCTAA	2520

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RESULT 10
US-09-578-564A-6
/ Sequence 6, Application US/099785664
/ Publication No. US20030050241A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Borstein, David
/ APPLICANT: Denoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gertschen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Klabavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mackey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Tr
/ TITLE OF INVENTION: Acids Encoding
/ FILE REFERENCE: P2630F1C25
/ CURRENT APPLICATION NUMBER: US/09/9
/ CURRENT FILING DATE: 2001-10-16
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30

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; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 2945; DB 10; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GATCGGTTTGTGTCGCCCTGGGCATCAACAAATAGCCATCGACTTCGGGGAGCAGC 180

QY 181 CTTGACCGGGCATGTGCTGTCAGAGGATCGAGTCAGATGCTGCGCCAGCTACGG 240
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; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630F1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 2945; DB 10; Length 2945;
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Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1501 AGACATGCTCCGACAGAGGAGTGCAGACATCGTGGAAATGAGAGAGAGATGAATA 1560
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Qy 1741 GGGGACCTAGTGAATGTCTTTTACTGTGTCTATGTATATAAAACAAACGAAACAACTGACTT 1800
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Qy 2161 GACTGTGACCAAGCTGCTCAGTTCTCACCCCGACCGTGTATATACATGAGTACTTCT 2220
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Qy 2221 AAATGCCCGGGGAGCAAACTGACATGTTTGAATGATAGATTTTCACTCTGCGTCTC 2280
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Qy 2401 GGCTTGCTTTTCCCTCGCTTCTCCTGAAAGTCCGATTTAGAGCGAGTCAATGAGGATCC 2460
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Qy 2461 TAACCTTTGCAATTTTAGTTTTTACAGTGAAGCTTTTAAAGTCTCATCCAGCATTTCTAA 2520
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Qy 2521 TGCCAGGTTGCTGAGGGTAACTTTTGAAGTATATTTACCTGGTCTGCTATCCTTA 2580
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Qy 2581 GTCATAACTCTGCGGTACAGGTAATGAGATGTTACTACGTTACTTCCCTCCACACCAT 2640
Db 2581 GTCATAACTCTGCGGTACAGGTAATGAGATGTTACTACGTTACTTCCCTCCACACCAT 2640
Qy 2641 ACAGTAAAGCAAGACATTTTATTAACGATACAGAGTCACTATGTGTGCTCCCTGAAATA 2700
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Qy 2701 ACGATTTGCAATTCATGCGAGTGCAGTATATTTTCTAAAGTTTGGAAAGCAGGTTTTT 2760
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QY	2761	CCCTTAAAAAATTTAGACACGGTTCCTAAATGATTTAGTCAGAAATTCCTAGACTGA	2820	PRIOR FILING DATE: 1998-03-12
				PRIOR APPLICATION NUMBER: 60/078004
Db	2761	CCCTTAAAAAATTTAGACACGGTTCCTAAATGATTTAGTCAGAAATTCCTAGACTGA	2820	PRIOR FILING DATE: 1998-03-13
				PRIOR APPLICATION NUMBER: 60/078886
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				PRIOR APPLICATION NUMBER: 60/078936
Db	2821	AGAACCTAAACAAACAAAAATATTTTAAAGATATAATAATATGCTGTATATGTTATGTAAT	2880	PRIOR FILING DATE: 1998-03-20
				PRIOR APPLICATION NUMBER: 60/078910
QY	2881	TTATTTTAGCTTATATATACATTTCTCTATTTTCGCAATTTTCAATTAATTAATGTCCTTAATACA	2940	PRIOR FILING DATE: 1998-03-20
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Db	2881	TTATTTTAGCTTATATATACATTTCTCTATTTTCGCAATTTTCAATTAATTAATGTCCTTAATACA	2940	PRIOR FILING DATE: 1998-03-20
				PRIOR APPLICATION NUMBER: 60/079294
QY	2941	AAAAA 2945		PRIOR FILING DATE: 1998-03-25
				PRIOR APPLICATION NUMBER: 60/079656
Db	2941	AAAAA 2945		PRIOR FILING DATE: 1998-03-26
				PRIOR APPLICATION NUMBER: 60/079664

RESULT 13

US-09-978-824-6

; Sequence 6, Application US/09978824

; Publication No. US20030055216A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C14

; CURRENT APPLICATION NUMBER: US/09/978,824

; CURRENT FILING DATE: 2001-10-17

; PRIOR APPLICATION NUMBER: 09/918595

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-23

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

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RESULT 14

US-09-918-585A-6
; Sequence 6, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavind, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PICI
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-03-25
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
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PRIOR APPLICATION NUMBER: 60/079689
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
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US-09-978-423A-6

; Sequence 6, Application US/09978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C21

; CURRENT APPLICATION NUMBER: US/09/978,423A

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; PRIOR FILING DATE: 2001-07-30

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(without alignments)
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	43.4	1.5	11474	4	US-09-495-406-1
6	43.2	1.5	1230025	4	US-09-198-452A-1
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13	41.4	1.4	353	4	US-09-621-976-18033
14	41.4	1.4	5152	4	US-10-204-708-73
15	41	1.4	734	3	US-09-014-583-1
16	41	1.4	1377	4	US-09-252-991A-11683
17	41	1.4	1536	4	US-09-252-991A-11555
18	41	1.4	1667	1	US-08-485-284A-1
19	40.8	1.4	4403765	3	US-09-103-840A-2
20	40.8	1.4	4411529	3	US-09-103-840A-1
21	40.6	1.4	1041	4	US-09-252-991A-5300
22	40.6	1.4	1341	4	US-09-252-991A-5263
23	40.4	1.4	3826	4	US-09-302-620B-90
24	40.4	1.4	3826	4	US-09-912-161-13
25	40.4	1.4	1664976	4	US-08-916-421B-1
26	40.2	1.4	9636	1	US-08-323-170B-1
27	40.2	1.4	9636	4	US-08-954-441-1

28	40	1.4	19233	4	US-10-204-708-46	Sequence 46, Appl
29	39.8	1.4	414	4	US-09-891-641-13	Sequence 13, Appl
30	39.8	1.4	507	4	US-09-252-991A-2433	Sequence 2433, Ap
31	39.8	1.4	840	4	US-09-252-991A-2594	Sequence 2594, Ap
32	39.8	1.4	1275	4	US-09-252-991A-2324	Sequence 2324, Ap
33	39.8	1.4	1527	4	US-09-252-991A-2252	Sequence 2252, Ap
34	39.6	1.3	3138	1	US-07-867-106-4	Sequence 4, Appli
35	39.4	1.3	837	3	US-08-998-416-288	Sequence 288, App
36	39.4	1.3	4521	4	US-09-533-494A-18	Sequence 18, Appl
37	39.4	1.3	8920	2	US-08-446-855A-1	Sequence 1, Appli
38	39.4	1.3	8920	3	US-09-150-741-1	Sequence 1, Appli
39	39	1.3	734	3	US-09-014-583-1	Sequence 1, Appli
40	39	1.3	1667	1	US-08-485-284A-1	Sequence 5, Appli
41	39	1.3	1712	4	US-09-144-776B-5	Sequence 7, Appli
42	39	1.3	1712	4	US-09-144-776B-7	Sequence 3, Appli
43	39	1.3	3232	4	US-09-333-214-3	Sequence 3, Appli
44	38.8	1.3	3003	4	US-09-252-991A-14790	Sequence 14790, A
45	38.8	1.3	3132	4	US-09-252-991A-14540	Sequence 14540, A

ALIGNMENTS

RESULT 1
US-09-489-847-44
; Sequence 44, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2527)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-44

Query Match 79.2%; Score 2332.2; DB 4; Length 2572;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2345; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY	595	TCAGGTGTTGTTTGTAGCCATTTCCTTCACAGTCACCTGGATCGCGGAGCCCTGCT	654
DB	40	TCAGGTGTTGTTTGTAGCCATTTCCTTCACAGTCACCTGGATCGCGGAGCCCTGCT	99
QY	655	CATCCCGATCCCTCTCTTGTACATGGCGCATTTGTGGCTGCACACCTGTGCTGGG	714
DB	100	CATCCCGATCCCTCTCTTGTACATGGCGCATTTGTGGCTGCACACCTGTGCTGGG	159
QY	715	CTACTACAGACATTCACGACATCATCCTCAGACAGATGCCCGGAGCTGGGGGAGA	774
DB	160	CTACTACAGACATTCACGACATCATCCTCAGACAGATGCCCGGAGCTGGGGGAGA	219

775 TGCAACAATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAAATCTTGGCCACACA 834
220 TGCAACAATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAAATCTTGGCCACACA 279
835 GAGAAATCAGTCGGGCTATTGTCAACCTCTTTGTTTCCGGGAGCCTTGGTGGCAGTTCTGC 894
280 GAGAAATCAGTCGGGCTATTGTCAACCTCTTTGTTTCCGGGAGCCTTGGTGGCAGTTCTGC 339
895 AGCCACAGAGGCACTGGGGAATTTTGACAGCCACATACCTGTGGGTGCATATGCCATACGG 954
340 AGCCACAGAGGCACTGGGGAATTTTGACAGCCACATACCTGTGGGTGCATATGCCATACGG 398
955 CTGGTTGACGAAATCGGTGCTGTATCTCTGCTTTGCAAGAAATACCCAGCAACAA 1014
399 CTGGTTGACGAAATCGGTGCTGTATCTCTGCTTTGCAAGAAATACCCAGCAACAA 458
1015 ACTGGTAGCAGGACGACAAACAGTCACGGCAGCCACATCAAGAAATCTCTGCTG 1074
459 ACTGGTAGCAGGACGACAAACAGTCACGGCAGCCACATCAAGAAATCTCTGCTG 518
1075 CATGGCTCTGTCACTACGCTCTGTTTCGTGATGTTTTGGACACCCCAAGTGTCTGAGAA 1134
519 CATGGCTCTGTCACTACGCTCTGTTTCGTGATGTTTTGGACACCCCAAGTGTCTGAGAA 578
1135 AATCTTGATAGACATCATCGGAGTGGACTTTGCCCTTTGCAGAACTCTGTGTTCTCTTT 1194
579 AATCTTGATAGACATCATCGGAGTGGACTTTGCCCTTTGCAGAACTCTGTGTTCTCTTT 638
1195 GCGGATCTTCTCTTCTCCAGTTCAGTCCAGTGGAGGCGCATCTCACCGGGTGGCT 1254
639 GCGGATCTTCTCTTCTCCAGTTCAGTCCAGTGGAGGCGCATCTCACCGGGTGGCT 698
1255 GATGACACTGAAGAAAACTTCTGCTTGGCCCAAGCTCTGTGCTGGGATCATCGTCCCT 1314
699 GATGACACTGAAGAAAACTTCTGCTTGGCCCAAGCTCTGTGCTGGGATCATCGTCCCT 758
1315 CATGGCAGCTCTGCTCTACCTTCTGCGGTGACCGGTGGACCCCTGGGCTGGG 1374
759 CATGGCAGCTCTGCTCTACCTTCTGCGGTGACCGGTGGACCCCTGGGCTGGG 818
1375 CTCCCTCTCTGGGGCTTTGTGGGAGATCCACCATGCTCGCATCGCTGGTGTCTATGT 1434
819 CTCCCTCTCTGGGGCTTTGTGGGAGATCCACCATGCTCGCATCGCTGGTGTCTATGT 878
1435 CTACCGGAGGCAAGAAAAATGAGAGATGAGTGGCCACCGGAGGGAAGACTCTGC 1494
879 CTACCGGAGGCAAGAAAAATGAGAGATGAGTGGCCACCGGAGGGAAGACTCTGC 938
1495 CATGACAGACATGCTCCGACAGAGGAGTGCACACATCGTGGAAATGAGAGAGGAA 1554
939 CATGACAGACATGCTCCGACAGAGGAGTGCACACATCGTGGAAATGAGAGAGGAA 998
1555 TGAATAAGGACAGGAGCGGATGGGCACTGCGAGGAGCGTCAAGTCAAGATGACATTCGG 1614
999 TGAATAAGGACAGGAGCGGATGGGCACTGCGAGGAGCGTCAAGTCAAGATGACATTCGG 1058
1615 CATCATCTCTCCCTCTCCCATGATTTGTTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTT 1674
1059 CATCATCTCTCCCTCTCCCATGATTTGTTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTT 1118
1675 GAAAGAGGCTTGATTTAAAGTTTGGTGTCAATCTCTAGCATACTGGGTATGCTCACA 1734
1119 GAAAGAGGCTTGATTTAAAGTTTGGTGTCAATCTCTAGCATACTGGGTATGCTCACA 1178
1735 CTGACGGGGGACCTAGTGAATGCTTTTACTGCTGCTATGTAAGAAACAAAGCAACAAAC 1794
1179 CTGACGGGGGACCTAGTGAATGCTTTTACTGCTGCTATGTAAGAAACAAAGCAACAAAC 1238
1795 TGAATTCATACCCCTGCTCAGGAAACCCCAAGACACAGCTGCTCTACGGTTCAGCTT 1854
1239 TGAATTCATACCCCTGCTCAGGAAACCCCAAGACACAGCTGCTCTACGGTTCAGCTT 1298
1855 GTGTCTCTCTCCCTGACAAATCTCTCTCTTGGAAACCAAGGACTGCGAGCTGTGCCATCGC 1914

Db 1299 GTGTCTCTCTCCCTGGGACATCTCTCTTGGAAACCAAGGACTGCGAGCTGTGCCATCGC 1358
Qy 1915 GCCTCGGTACCTGTGCAGAGGCGACAGACTCTCTCTGTGCCCCCTTTCATCGCTCTTAAG 1974
Db 1359 GCCTCGGTACCTGTGCAGAGGCGCGACAGACTCTCTCTGTGCCCCCTTTCATCGCTCTTAAG 1418
Qy 1975 AATCAACAGGTTAAACCTCGGCTTCTCTTTGATTTGCTTCCAGGTCACATGCGCGGTACAAA 2034
Db 1419 AATCAACAGGTTAAACCTCGGCTTCTCTTTGATTTGCTTCCAGTCACATGCGCGGTACAAA 1478
Qy 2035 GAGATGGAGCCCGGTGGCTCTCTTAAATTTCCCTTCTGCGCAGCGAGTTGCAAAACCATCTA 2094
Db 1479 GAGATGGAGCCCGGTGGCTCTCTTAAATTTCCCTTCCGCGCAGGAGTTGCAAAACCATCTA 1538
Qy 2095 CTCACACATGAGAGGCGGTGGCAGCTGCGACCGCGGAGTCCCGCTTCCACATGAGG 2154
Db 1539 CTCACACATGAGAGGCGGTGGCAGCTGCGACCGCGGAGTCCCGCTTCCACATGAGG 1598
Qy 2155 AACGGAGCCTGTGACCAAGCAGCGCTGCAGATGGAAGATCTCCCGTGAAAGGTTT 2214
Db 1599 AACGGAGCCTGTGACCAAGCAGCGCTGCAGATGGAAGATCTCCCGTGAAAGGTTT 1658
Qy 2215 GGTTTGAAATGCCCGGGGCGAGCAAACTGACATGTTGAATGATAGCATTTCACTCTGC 2274
Db 1659 GGTTTGAAATGCCCGGGGCGAGCAAACTGACATGTTGAATGATAGCATTTCACTCTGC 1718
Qy 2275 GTTCTCCTAGATCTGAGCAAGCTGTCAAGCTTCTCAAGCTGATATATATAGCTA 1778
Db 1719 GTTCTCCTAGATCTGAGCAAGCTGTCAAGCTTCTCAAGCTGATATATATAGCTA 1778
Qy 2335 ACTTTTTTAAATGTGCACAAAGCGCATCTCCAGATTTCCAGACCCCTGCCGATGACTTTT 2394
Db 1779 ACTTTTTTAAATGTGCACAAAGCGCATCTCCAGATTTCCAGACCCCTGCCGATGACTTTT 1838
Qy 2395 CTTGAAGGCTTGCTTTTCCCTCGCTTCTGAAAGTGCATTTAGAGCGAGTCACATGGA 1898
Db 1839 CTTGAAGGCTTGCTTTTCCCTCGCTTCTGAAAGTGCATTTAGAGCGAGTCACATGGA 1898
Qy 2455 GCATCTTAATTTGCAATTTTACGTTTACGTTGAACTGAAGCTTTAAAGTCTCATCCAGCA 2514
Db 1899 GCATCTTAATTTGCAATTTTACGTTTACGTTGAACTGAAGCTTTAAAGTCTCATCCAGCA 1958
Qy 2515 TTCTAATGCGAGGTTGCTGTAGGTTAACTTTTGAAGTATATATATATATATATATATATAT 2574
Db 1959 TTCTAATGCGAGGTTGCTGTAGGTTAACTTTTGAAGTATATATATATATATATATATATAT 2018
Qy 2575 TCTTAGTCTAATCTCTGCGGTACAGTAAATTCAGAAATGTAAGTCTTCTAGTCTTCTCCCTCA 2634
Db 2019 TCTTAGTCTAATCTCTGCGGTACAGTAAATTCAGAAATGTAAGTCTTCTAGTCTTCTCCCTCA 2078
Qy 2635 CACCATACGATAAAGCAAGACATTTTATACGATACCGAGTCACTATGTGTTCTCTCCCT 2694
Db 2079 CACCATACGATAAAGCAAGACATTTTATACGATACCGAGTCACTATGTGTTCTCTCCCT 2138
Qy 2695 GAAATAACGATTCGAAATCCATTCGAGTGCAGTATATTTTCTAAGTTTGGAAAGCGG 2754
Db 2139 GAAATAACGATTCGAAATCCATTCGAGTGCAGTATATTTTCTAAGTTTGGAAAGCGG 2198
Qy 2755 TTTTTTCTTTTAAATAAATATAGACAGGTTCACTAAATTTAGTTAGTCAGAAATTCCTA 2814
Db 2199 TTTTTTCTTTTAAATAAATATAGACAGGTTCACTAAATTTAGTTAGTCAGAAATTCCTA 2258
Qy 2815 GACTGAAAGAACCTTAAACAAAAAATTTTAAAGATATAAATATATATATATATATATATAT 2874
Db 2259 GACTGAAAGAACCTTAAACAAAAAATTTTAAAGATATAAATATATATATATATATATATAT 2318
Qy 2875 TGTAAATTTATTTAGGCTATAATACATTTCTCTATTTTTCGCAATTTTCAATAAATGCTCT 2934
Db 2319 TGTAAATTTATTTAGGCTATAATACATTTCTCTATTTTTCGCAATTTTCAATAAATGCTCT 2378
Qy 2935 AATACAAA 2943
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QY 1560 AAGCAGCGGAGCCATGGGCACTGAGGAGCGGTAGTCAGGATGACACTTCGGCATCA 1619
Db 1122 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCG 1063
QY 1620 TCTCTTCCCTCTCC 1634
Db 1062 CAAGTCCCTCGACC 1048

RESULT 4
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

Query Match 1.5%; Score 43.6; DB 4; Length 640681;
Best Local Similarity 54.5%; Pred. No. 3.7;
Matches 109; Conservative 0; Mismatches 89; Indels 2; Gaps 1;

QY 2729 TATTTTCTAGTTTGGAAAGCAGGTTTTTCCTTTAAATAAATTTATAGACACGGTTCA 2788
Db 32533 TTTTATTGAATGTTTGTGAATATATCAATTGAAATAAATAATTTTATTATCGATCG 325474

QY 2789 CT-AAATGATTAGTCAGATTCCTAGACTGAAAGCAACCTAAACAAAAAATATTTTTA 2846
Db 325473 ATGCAATTCITTTTATATAAAATTAGATAAATAAAGAAATTCATCCITTATTTA 325414

QY 2847 AAGATATAAATATGCTGTATGTTATGTAATTTATTTAGCTATAATACATTTTCT 2906
Db 325413 TTTATATTGATAAATTTTTTGTCTTTATTTTACTTATTTTATTATATACTATAATATC 325354

QY 2907 ATTTTCGCATTTTCAATAAA 2926
Db 325353 ATTATAGTAATTTAAAAAAA 325334

RESULT 5
US-09-495-406-1
; Sequence 1, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
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; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-09-495-406-1

Query Match 1.5%; Score 43.4; DB 4; Length 11474;
Best Local Similarity 51.9%; Pred. No. 0.37;
Matches 98; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 2757 TTTTCCCTTTAAAAAATTTATAGACACGGTTCACTAAATTTAGTCAGAAATTCCTAGA 2816
Db 3913 TTATGATATTTGGAAATTTTGCACAAAAATAAATAATTTTAAATAAATAATATAAAAA 3972

QY 2817 CTGAAAGAACCTAAACAAAAAATTTTAAAGATATAAATAATATGCTGTATATGTTATG 2876
Db 3973 ATTAATTAATTTTAGGTATATACATATAATTTAGGAGAAATATTTTATATGCTATT 4032

QY 2877 TAATTTATTTAGGCTATAATACATTTCTTATTTTCCGATTTTCAATAAAATGCTCTAA 2936
Db 4033 TCAATCATACITTTGTGAAAAATAATTTGCTTATTCATCCCTTTTAGAAAAATTTAGACATAA 4092

QY 2937 TACAAAAA 2945
Db 4093 AATAAAAA 4101

RESULT 6
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment;
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev;
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (105001)..(120000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (120001)..(135000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

Query Match 1.4%; Score 43.2; DB 4; Length 1230025;
Best Local Similarity 52.2%; Pred. No. 7.1;
Matches 96; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 2710 AATCCATGAGGAGTATATTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAA 2769
DB 110233 AATCTTGAAATGAAGATCTTTTCAGATAGATGAGATGATTTTATATA 1109174
QY 2770 AATTATAGACGGTTCTACTAAATGATTAGTCAGAAATTCCTAGACTGAAGAACTA 2829
DB 1109173 AATGCTAAACCTGAAGAGGATCTCTGCTGAAATGTTTCTGAGATTTCAAGATCTC 1109114
QY 2830 AACCAAAAATATTTTAAAGATATAATATATGCTGTATGTTATGTAATTTTATAG 2889
DB 1109113 AGAATAGCTGCTACTGCACTTCAGACTTTTAGGAGATCTGATGAACCTTCTTAAG 1109054
QY 2890 GCTA 2893
DB 1109053 GCCA 1109050

RESULT 7

US-09-489-039A-2573/c
Sequence 2573; Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2573
LENGTH: 1302
TYPE: DNA
ORGANISM: Klebsiella pneumoniae

US-09-489-039A-2573

Query Match 1.4%; Score 42.6; DB 4; Length 1302;
Best Local Similarity 53.3%; Pred. No. 0.16;
Matches 90; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1249 GTGGCTCATGACACTGAAGAAACCTTCGTCCTGGCCCGACGCTCTGTGCTCGGATCAT 1308
DB 856 GTGATGCCGAGCGGAGAGAGATCTTCGCTTCGCCACATGTCGTGGGATGTTTAT 797
QY 1309 GTGCTCATGCGACGCTCTGTGCTCTACCTTACCTTGGGGTGCAGGTGGACCCCTGGG 1368
DB 796 TGGCCTTATCGACATCCAGATCGTCTCCGCTCGCTGCGGATATTGGCGGCGCTGTC 737
QY 1369 CGTGGGCTCCTCTCTGGCGGGCTTTTGGGAGAAATCCACCATGTCGCC 1417
DB 736 GCGGGCGGAGATGAACCTCTGGGTACAAACCACTACCTGATGCC 688

RESULT 8

US-09-489-039A-2262
Sequence 2262; Application US/09489039A
Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2262
LENGTH: 1617
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2262

Query Match 1.4%; Score 42.6; DB 4; Length 1617;
Best Local Similarity 53.3%; Pred. No. 0.19;
Matches 90; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1249 GTGGCTCATGACACTGAAGAAACCTTCGTCCTGGCCCGACGCTCTGTGCTCGGATCAT 1308
DB 93 GTCGATGCCGAGCGGAGAAAGATCTTCGCTTCGCCAGCATGTGCTGGGATGTTTAT 152
QY 1309 CGTCCTCATGCGACGCTCTGTCCTACCTTACCTGCGGTGCGGTGCGACGTCGACCCCTGGG 1368
DB 153 TGCCTTATCGACATCCAGATCGTCTCGCTCGCTGCGGATATTGGCGGCGCTGTC 212
QY 1369 CGTGGGCTCCTCTCTGGCGGGCTTTGTGGGAGATCCACCATGTCGCC 1417
DB 213 GCGGGCGGAGATGAACCGTCTGGGTACAAACCACTACCTGATGCC 261

RESULT 9

US-09-790-988-1
Sequence 1; Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1

LENGTH: 640681

TYPE: DNA
ORGANISM: Buchnera sp.

US-09-790-988-1

Query Match 1.4%; Score 42.6; DB 4; Length 640681;
Best Local Similarity 50.2%; Pred. No. 7;
Matches 105; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 2727 TATATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAATATAGACACGGTT 2786
DB 355415 TATATAAATACCTAGTAATAATAATATTTATTTTATTAAGTTCTTTAGTAAAT 355474
QY 2787 CACTAAATGATTTAGTCAGAAATTCCTAGACTGAAAGAACCTAAACAAAAAATATTTTA 2846
DB 355475 AATTATAATAATTTTTTTTATAGTAAATATAGAAAAACATTAATATATATTTTA 355534
QY 2847 AGATATAAATATGCTGTATATGTTATGTAATTTTATTTAGGCTATAATACATTTCT 2906
DB 355535 AAAAAATGTTATATTTTAAACAGTTTATATAAATCATTCCTCAAAACCGCAATTTAA 355594
QY 2907 ATTTGCGATTTTCAATAAAATGTCCTA 2935

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Db 355595 ATTATGCAATTAATAATTTTAAATTTTATA 355623
|||||
RESULT 10
US-08-487-826B-13/C
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; APPLICANT: Willems, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match 1.4%; Score 42; DB 2; Length 19124;
Best Local Similarity 52.9%; Pred. No. 1.2;
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 2728 ATATTTTCTAAGTTTGGAAAGCAGGTTTTCCTTTTAAAGAAATTTATAGACACGGTTC 2787
Db 1491 AAATGTTTGAAGTTTAAAGCAATTTATTTATTTAAATACTAAATCATATAATTA 1432
QY 2788 ACTAATTTGATTGTAGTCAGATTCTGACTGGAAGAACCTTAAACAAAAAATATTTTAA 2847
Db 1431 TGAATAAATAATATATATATTTATTTATTTTAAATAAATAAAGAGAGACAAATTA 1372
QY 2848 AGATAATAATATGCTGTATATGTTATGTAATTTATTTTAAAGGCTATAAT 2897
Db 1371 AATAAAAAAGATATATATATATATATATATATATATATATATATATATATATATAT 1322

RESULT 11
US-09-601-198-153
; Sequence 153, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Casseil, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
; US-09-601-198-153

Query Match 1.4%; Score 41.8; DB 4; Length 1866;
Best Local Similarity 50.8%; Pred. No. 0.34;
Matches 100; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 2686 GTCCTCCCTGAAATACGCATTCGAAATCCATGCGATGCCAGTATATTTTCTAAGTTTG 2745
Db 1019 GTGATCATTTTATGACAAATGAAAAAACAACAAAAATAGAAATTTTAGATCTTTTG 1078
QY 2746 GAACGACGTTTTCCTTTTAAAAAATATAGACACGGTTCCTAAATTTAGTCA 2805
Db 1079 ATAAAGAAATCGAATTTTTCARAAATATATTTGATCATTAATTTAGATTTAATA 1138
QY 2806 GAATTCCTAGACTGAAAGACCTTAAACAAAAAATTTTAAAGATATAAATATATGCTG 2865
Db 1139 AAATTTCAAGGACGATATATTACACAAAAAATAATTTAAAAATCTTTTATTAGATGCTT 1198
QY 2866 TATATGTTATGTAATTT 2882
Db 1199 TCAATAATAATGATGTT 1215

RESULT 12
US-09-621-976-18033/C
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Gobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
; US-09-621-976-18033

Query Match 1.4%; Score 41.6; DB 4; Length 474;
Best Local Similarity 13.8%; Pred. No. 0.17;
Matches 44; Conservative 135; Mismatches 139; Indels 0; Gaps 0;

QY 2465 TTTCGATTTTAGTTTTCAGTGAAGCTTAAAGTCTCATCCAGCATTTCTAATGCC 2524
|||||
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Db 377 WTTWACCCYTTTWWKMMMYTTKRRRWRGRKWTCTYTAWSKYVWYSRWKKGRAAMYK 318
QY 2525 AGTTCTGCTAGGTAACCTTTTGAAGTAGATATATACCTGGTCTGTATCCTTAGTCA 2584
Db 317 RRGKYNRRARWTTWARRAMYTWTYWKSGSWKMSMKWKRYKWKCCYWWRRKYC 258
QY 2585 TAATCTGCGGTACAGTAATAGAGTAATGACTACGGTACTTCCCTCCACACCATACGA 2644
Db 257 CMKRRRRGKRRARSYKSGSYVYKGGKGGTGKGGKMSKGRRRATTTTYYK 198
QY 2645 TAAAGCAGACATTTTATACGATACACAGTCACTATGCTGCTCCTCGAATAAGC 2704
Db 197 KKWRSYWAARGKTTTKWAAWMMCMWYMSMMYYKWAAWKSCCWRRKGGSG 138
QY 2705 ATTCGAATCCAGTCAGTGCATATATTTTCTAAAGTTTGGAAAGCAGGTTTTTCTT 2764
Db 137 RYWKRRGTCMRGRWYRRRMCWYCTKSMAMMSGKKRAAMCCSKYYVWMCMA 78
QY 2765 TAAAAAATTTATAGAC 2782
Db 77 AAAAATTTAAAAAAMRS 60

RESULT 13

US-09-621-976-9783/c
; Sequence 9783, Application US/09621976
; Patent No. 6539063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9783
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9783

Query Match 1.4%; Score 41.4; DB 4; Length 353;

Best Local Similarity 50.4%; Pred. No. 0.16; Mismatches 101; Indels 0; Gaps 0;

Matches 102; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 2728 ATATTTTCTAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAATTATAGCAGGTC 2787
Db 309 ATGTAATTTAAAGTTGCAATGAAGCAATTACAGAAATATAATATGCTATATCTCTC 250
QY 2788 ACTAAATTTAGTATAGTCAATCTTCTAGCTGAAGACCTAAACAAAAAATATTAA 2847
Db 249 TATACCTGAATGATTTCAATTAATAAATGATCTGATCTTTAAACATGAATATTC 190
QY 2848 AGATATAAATATATGCTGTATATGTTATGTTATTTTATTTAGCTATATATCTCTA 2907
Db 189 AGATATGATCTATCTCTGTTATTTTAAAAAATCACTTTAGCAATATTTTACATA 130
QY 2908 TTTTCGATTTTCAATAAATGT 2930
Db 129 CAATAATGTATCTATTCAGTGT 107

RESULT 14

US-10-204-708-73
; Sequence 73, Application US/10204708
; Patent No. 6577731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/BF01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-73

Query Match 1.4%; Score 41.4; DB 4; Length 5152;
Best Local Similarity 53.0%; Pred. No. 0.81;
Matches 133; Conservative 0; Mismatches 116; Indels 2; Gaps 2;

QY 2694 TGAATAACGCATTCGAATCCATCGCAGTGCAGTATATTTTCTAAGTTTGGAAAGCAG 2753
Db 3345 TGAATAATGTTATTTGTTATATTTTAAAAATTTTGTGTAAATATTTTAAATAT 3404
QY 2754 GTTTTTCCTTTAAAAAATATATAGACACGGTTCCTAAATTTGTTAGTCAGAAATTCCT 2813
Db 3405 TTCGTTAATATAAATAGTTTATTTTACGATTTTATTTAGT-ATTTAGAAAAAGAAAA 3463
QY 2814 AGCTGAAAGAACCTAAACAAAAAATATTTTAAAGATATAATA-TATGCTGTATATGT 2872
Db 3464 AAGAAAAAGTAAATTAAGTGAATTTAAAGTATTTTAAAGTATTTTAAATATATATGT 3523
QY 2873 TATGTAATTTATTTTGGCTATATACATTTTCCATTTTCCATTTTCCATTAATATCTCT 2932
Db 3524 TATTAGAAAAATAAGTGTGTTTATATTTTATTTTATTTAGTTTAAAGGAGATTTTATTAATTT 3583
QY 2933 CTAAATACAAA 2943
Db 3584 TTAATAAAGA 3594

RESULT 15

US-09-014-583-1
; Sequence 1, Application US/09014583
; Patent No. 6140077
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Takeshi
; APPLICANT: SUZUKI, Tadashi
; APPLICANT: TOKUDA, Junko
; APPLICANT: KATO, No. 6140077uo
; APPLICANT: SAKAI, Yasuyoshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: TAKAHASHI, Hitoshi
; TITLE OF INVENTION: METHOD FOR PRODUCING PHYLASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Mon Apr 26 07:58:59 2004

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/014,583

FILING DATE: 28-JAN-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 200398/96

FILING DATE: 30-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 027066-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 734 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Candida boidinii

DEVELOPMENTAL STAGE: wild type

US-09-014-583-1

Query Match 1.4%; Score 41; DB 3; Length 734;

Best Local Similarity 49.3%; Pred.No. 0.32; Indels 0; Gaps 0;

Matches 107; Conservative 0; Mismatches 110;

Qy 2728 ATATTTTCTAAGTTTGGAAAGCAGGTTTTTTCCTTTTAAAAAATTATAGACACGGTTC 2787

Db 429 AAAAATTATATTTAAATGAATTAATTCCTTTATTTTAAATAATATCGTTAATTCCTTTA 488

Qy 2788 ACTAATTTGATTTAGTCAGNATTCCTAGACTGAAAGACCTAAACAAAAATATTTTAA 2847

Db 489 AATTCATTTTATTTTAAATTCCTTTATCATAGTATCATATAACAATTTATTAACAT 548

Qy 2848 AGATAAAATATATGCTATATATGTAATTTATTTAGGCTATAATACATTTTCCTA 2907

Db 549 AGATACACATTTATTTTATTTATCATATTTATTTTAAATATTTGATTATTTTAAAAA 608

Qy 2908 TTTTCGCAATTTCAATAAAATGCTCTAATACAAAAA 2944

Db 609 TAATATCTTAATTAATTAATTTTACGAATATACAAA 645

Search completed: April 25, 2004, 17:25:23

Job time : 230 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 12:30:23 ; Search time 1123 Seconds
(without alignments)
11140.644 Million cell updates/sec

Title: US-09-978-188A-6
Perfect score: 2945
Sequence: 1 cgtcgcccgctgcccctc.....aatgtctctatacaaaaaa 2945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2945	100.0	2945	2 AAZ33895	Aaz33895 Human PRO
2	2945	100.0	2945	3 AAC78459	Aac78459 Human PRO
3	2945	100.0	2945	6 ABK40261	Abk40261 cDNA enco
4	2945	100.0	2945	7 ACD42428	Acd42428 Novel hum
5	2945	100.0	2945	7 ACA63463	Aca63463 Novel hum
6	2945	100.0	2945	7 ACA71627	Aca71627 Human sec
7	2945	100.0	2945	7 ABX92267	Abx92267 cDNA enco
8	2945	100.0	2945	7 ACA66008	Aca66008 Human cDN
9	2945	100.0	2945	8 ADA24545	Ada24545 Novel hum
10	2945	100.0	2945	8 ACD29609	Acd29609 Novel hum
11	2945	100.0	2945	8 ADA12206	Ada12206 Human cDN
12	2945	100.0	2945	8 ACD29024	Acd29024 Novel hum
13	2945	100.0	2945	9 AD873512	Ad873512 Human PRO
14	2945	100.0	2945	9 AD876228	Ad876228 Human PRO
15	2945	100.0	2945	9 ADC43654	Adc43654 Human cDN
16	2945	100.0	2945	9 ADC61414	Adc61414 Human cDN
17	2945	100.0	2945	9 ADC63378	Adc63378 Human cDN
18	2945	100.0	2945	9 ADC66478	Adc66478 Human cDN
19	2945	100.0	2945	9 ADC68602	Adc68602 Human cDN
20	2945	100.0	2945	9 ADC62662	Adc62662 Human cDN
21	2945	100.0	2945	9 ADC67727	Adc67727 Human cDN
22	2945	100.0	2945	9 ADC41047	Adc41047 Human cDN
23	2945	100.0	2945	9 ADC67102	Adc67102 Human cDN

24	2945	100.0	2945	9 ADC62038	Adc62038 Human cDN
25	2945	100.0	2945	9 ADC41671	Adc41671 Human cDN
26	2945	100.0	2945	9 ADE49040	Ade49040 Human cDN
27	2945	100.0	2945	9 ADE35094	Ade35094 Human cDN
28	2945	100.0	2945	9 ADE18208	Ade18208 Human cDN
29	2945	100.0	2945	9 ADD72823	Add72823 Human cDN
30	2945	100.0	2945	9 ADD72181	Add72181 Human cDN
31	2945	100.0	2945	9 ADE16832	Ade16832 Human cDN
32	2945	100.0	2945	10 ADE48340	Ade48340 Human cDN
33	2945	100.0	2945	10 ADE89441	Ade89441 Human cDN
34	2756.6	93.6	2986	4 AAI59695	Aai59695 Human pol
35	2756.6	93.6	2986	9 ADE09752	Ade09752 Novel DNA
36	2747.6	93.3	3139	4 AAI59909	Aai59909 Human pol
37	2543.2	86.4	2744	6 ABL90359	Abi90359 Human sec
38	2332.2	79.2	2572	3 AAA26379	Aaa26379 Human sec
39	2332.2	79.2	2572	7 ADA56105	Ada56105 Gene enco
40	2332.2	79.2	2572	7 ADA39918	Ada39918 Human sec
41	2332.2	79.2	2572	7 ACC50502	Acc50502 Human sec
42	2332.2	79.2	2572	7 ABZ71278	Abz71278 Human sec
43	2332.2	79.2	2572	8 ADB91184	Adb91184 Human sec
44	2332.2	79.2	2572	9 ADC73564	Adc73564 Human sec
45	2146.6	72.9	2748	3 AAC77393	Aac77393 Human ORF

ALIGNMENTS

RESULT 1

AAZ33895
ID AAZ33895 standard; cDNA; 2945 BP.

XX AAZ33895;

DT 07-DEC-1999 (first entry)

XX Human PRO274 nucleotides sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein; ss.

XX Homo sapiens.

XX WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

XX 11-MAR-1998; 98US-0077641P.

XX 11-MAR-1998; 98US-0077649P.

XX 12-MAR-1998; 98US-0077791P.

XX 13-MAR-1998; 98US-0078004P.

XX 17-MAR-1998; 98US-00040220.

XX 20-MAR-1998; 98US-0078886P.

XX 20-MAR-1998; 98US-0078910P.

XX 20-MAR-1998; 98US-0078936P.

XX 20-MAR-1998; 98US-0078939P.

XX 25-MAR-1998; 98US-0079294P.

XX 26-MAR-1998; 98US-0079656P.

XX 27-MAR-1998; 98US-0079664P.

XX 27-MAR-1998; 98US-0079689P.

XX 27-MAR-1998; 98US-0079728P.

XX 27-MAR-1998; 98US-0079786P.

XX 30-MAR-1998; 98US-0079920P.

XX 30-MAR-1998; 98US-0079923P.

XX 31-MAR-1998; 98US-0080105P.

XX 31-MAR-1998; 98US-0080107P.

XX 31-MAR-1998; 98US-0080165P.

XX 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081223P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 21-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083493P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084411P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085123P.
PR 13-MAY-1998; 98US-0085138P.
PR 13-MAY-1998; 98US-0085239P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0085704P.
PR 22-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 28-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX (GETH) GENENTECH INC.
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX P-PSDB; AAY41686.
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
adhesion disorders.
XX Claim 2; Fig 3; 530pp; English.
XX The present invention describes secreted and transmembrane polypeptides
and their polynucleotides. The nucleotide sequences are useful as sources
of probes, primers, for chromosome mapping, and for generation of
antisense sequences. They can also be used to create transgenic animals.
The proteins can be used to treat a variety of diseases and disorders,
depending on their function. Diseases that may be treated include blood
coagulation disorders, cancers and cellular adhesion disorders. They may
also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
AAY41774 represent polynucleotide and polypeptide sequence given in the
exemplification of the present invention
XX Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 2945; DB 2; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCTCGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTG 60
DB 1 CGCTCGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTG 60
QY 61 GGCTCAGCCCAACCGCGGAGCTATGTGAAATCCCGGCGCTCACGACTACTGCCCCCT 120
DB 61 GGCTCAGCCCAACCGCGGAGCTATGTGAAATCCCGGCGCTCACGACTACTGCCCCCT 120
QY 121 GATCCGGTCTTGGTGGCTCCCTCGGCATCACCAATAGCATCGACTTCGGGAGCAGGC 180
DB 121 GATCCGGTCTTGGTGGCTCCCTCGGCATCACCAATAGCATCGACTTCGGGAGCAGGC 180
QY 181 CTTGAACCGGGCATTGCTGCTCAAGGAGGATGAGTCGAGATCGTGGCAGCTACCG 240
DB 181 CTTGAACCGGGCATTGCTGCTCAAGGAGGATGAGTCGAGATCGTGGCAGCTACCG 240
QY 241 GCTGGGTACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGG 300
DB 241 GCTGGGTACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGG 300
QY 301 CCTGGTGTGTAACAGCAAGAGAGACAGAGCCAAAGCCGCTCTGTATGTTGTTGTC 360
DB 301 CCTGGTGTGTAACAGCAAGAGAGACAGAGCCAAAGCCGCTCTGTATGTTGTTGTC 360
QY 361 AGGGCCATCGCTCCGCTCTTTCACACACTGATAGTATAGTATTAGGATACAT 420
DB 361 AGGGCCATCGCTCCGCTCTTTCACACACTGATAGTATAGTATTAGGATACAT 420
QY 421 TATCAATAAACTGCACCATGTGACGAGTGGTGGGAGCAAGACGAGAGGCGCTTCCT 480
DB 421 TATCAATAAACTGCACCATGTGACGAGTGGTGGGAGCAAGACGAGAGGCGCTTCCT 480
QY 481 GTACCTCGCGCTTTCCTTTTATGACGCAATGGATGGACCCATGCTGGCATTCCT 540
DB 481 GTACCTCGCGCTTTCCTTTTATGACGCAATGGATGGACCCATGCTGGCATTCCT 540
QY 541 AAAACACAAATACAGTTTCTCTGGTGGATGTGCTCAATCTCAGATGTCTAGTCAGGT 600
DB 541 AAAACACAAATACAGTTTCTCTGGTGGATGTGCTCAATCTCAGATGTCTAGTCAGGT 600
QY 601 TGTGTTGTAGCCATTTGCTTTCAGAGTACCTGGAAATGCGGGAGCCCTGCTCATCC 660
DB 601 TGTGTTGTAGCCATTTGCTTTCAGAGTACCTGGAAATGCGGGAGCCCTGCTCATCC 660
QY 661 GATCCTCTCTGTACATGGGCGCCTTGTGCGCTGCACCACCTGTGCTGGGCTACTA 720
DB 661 GATCCTCTCTGTACATGGGCGCCTTGTGCGCTGCACCACCTGTGCTGGGCTACTA 720
QY 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCCGAGAGTGGGGAGATGCAAC 780
DB 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCCGAGAGTGGGGAGATGCAAC 780

QY	781	AATAAGAAAGATGCTGAGCTTCTGGTGGCCCTTTGGCTCTAATTTCTGGCCACACAGAGAAT	840
DB	781	AATAAGAAAGATGCTGAGCTTCTGGTGGCCCTTTGGCTCTAATTTCTGGCCACACAGAGAAT	840
QY	841	CAGTGGCCCTATTGTTCAACCTCTTTGTTCCCGGACCTTGGTGGCAGTCTGCAGCCAC	900
DB	841	CAGTGGCCCTATTGTTCAACCTCTTTGTTCCCGGACCTTGGTGGCAGTCTGCAGCCAC	900
QY	901	AGAGGAGTGGCGAATTTGACAGCCACATACCTGTGGGTCAATGCCATACGGCTGGTT	960
DB	901	AGAGGAGTGGCGAATTTGACAGCCACATACCTGTGGGTCAATGCCATACGGCTGGTT	960
QY	961	GACGGAAATCGTCTGTGTATCTCTGCTTTGCGACAGAAATTAACCCAGCAACAACTGGT	1020
DB	961	GACGGAAATCGTCTGTGTATCTCTGCTTTGCGACAGAAATTAACCCAGCAACAACTGGT	1020
QY	1021	GAGCAGGAAACACAGTCAAGGAGCCACATCAAGAAAGTTCACCTTCGTCTGCATGGC	1080
DB	1021	GAGCAGGAAACACAGTCAAGGAGCCACATCAAGAAAGTTCACCTTCGTCTGCATGGC	1080
QY	1081	TCTGTCACTACGCTCTGTTTGTGATGTTTGTGACACCCAAACGTTGTCTGAGAAATCTT	1140
DB	1081	TCTGTCACTACGCTCTGTTTGTGATGTTTGTGACACCCAAACGTTGTCTGAGAAATCTT	1140
QY	1141	GATAGACATCATCGAGTGGACTTTGCTTTGCGAGAACTCTGTGTTGTTCTTTGCGGAT	1200
DB	1141	GATAGACATCATCGAGTGGACTTTGCTTTGCGAGAACTCTGTGTTGTTCTTTGCGGAT	1200
QY	1201	CTTCTCTCTTCTCCAGTTCAGTCAAGTGAAGGCGCATCTCACCGGGTGGCTGATGAC	1260
DB	1201	CTTCTCTCTTCTCCAGTTCAGTCAAGTGAAGGCGCATCTCACCGGGTGGCTGATGAC	1260
QY	1261	ACTGAGAAACCTTCGTCCTTGGCCAGCTCTGCTGGGATCATCGTCTCATCGC	1320
DB	1261	ACTGAGAAACCTTCGTCCTTGGCCAGCTCTGCTGGGATCATCGTCTCATCGC	1320
QY	1321	CAGCCTCGTGTCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT	1380
DB	1321	CAGCCTCGTGTCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT	1380
QY	1381	CCTGGCGGCTTTGTGGAGAAATCAACATGGTGGCCATCGCTGGTGTATGTTACCG	1440
DB	1381	CCTGGCGGCTTTGTGGAGAAATCAACATGGTGGCCATCGCTGGTGTATGTTACCG	1440
QY	1441	GAAAGAGAAAGAGATGAGATGAGTCTCGGCCACGAGGGGGAAGACTCTGCCATGAC	1500
DB	1441	GAAAGAGAAAGAGATGAGATGAGTCTCGGCCACGAGGGGGAAGACTCTGCCATGAC	1500
QY	1501	AGACATGCTCCGACAGAGGAGGTGACAGATCTGTGAAATGAGAGGAGAAATGAATA	1560
DB	1501	AGACATGCTCCGACAGAGGAGGTGACAGATCTGTGAAATGAGAGGAGAAATGAATA	1560
QY	1561	AGGACGGGACCCATGGSCATGAGGAGCGGTGAGTCAAGTCACTTCGGCATCAT	1620
DB	1561	AGGACGGGACCCATGGSCATGAGGAGCGGTGAGTCAAGTCACTTCGGCATCAT	1620
QY	1621	CTCTTCCCTCTCCCATCGTATTGTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGT	1680
DB	1621	CTCTTCCCTCTCCCATCGTATTGTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGT	1680
QY	1681	GGCCTTGATTAAGTTCGTTCTGATCTCTGACATCTGGGTATGCTCACATGACG	1740
DB	1681	GGCCTTGATTAAGTTCGTTCTGATCTCTGACATCTGGGTATGCTCACATGACG	1740
QY	1741	GGGGACCTTAGTGAATGGTCTTTACTGTTGCTATGTAAACAAACAAACAACTGACTT	1800
DB	1741	GGGGACCTTAGTGAATGGTCTTTACTGTTGCTATGTAAACAAACAAACAACTGACTT	1800
QY	1801	CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCACGGTTGACGTTGTGTC	1860
DB	1801	CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCACGGTTGACGTTGTGTC	1860

QY	1861	TCCTCCCTCGACAAATCTCTCTTTGGAAACCAAGGACTGCAGCTGTGCCATCGCCCTCG	1920
DB	1861	TCCTCCCTCGACAAATCTCTCTTTGGAAACCAAGGACTGCAGCTGTGCCATCGCCCTCG	1920
QY	1921	GTCAACCTTGACAGAGGCCACAGACTCTCTCTGTCGCCCTTCATCGCTCTTAAAGAAATCAA	1980
DB	1921	GTCAACCTTGACAGAGGCCACAGACTCTCTCTGTCGCCCTTCATCGCTCTTAAAGAAATCAA	1980
QY	1981	CAGGTTAAATCTCGGCTTCTCTTTGATTTGCTTCCAGTCACTGCGGTACAAAGAGATG	2040
DB	1981	CAGGTTAAATCTCGGCTTCTCTTTGATTTGCTTCCAGTCACTGCGGTACAAAGAGATG	2040
QY	2041	GAGCCCGGTCGCTCTTAAATTTCCCTTCTGCGACGGAGTTCGAAACCACTACTCCAC	2100
DB	2041	GAGCCCGGTCGCTCTTAAATTTCCCTTCTGCGACGGAGTTCGAAACCACTACTCCAC	2100
QY	2101	ACATGACAGAGCGGGTGGCGCTGCGACCGCGGAGTCCCCGTTCACTGAGGAGACGGA	2160
DB	2101	ACATGACAGAGCGGGTGGCGCTGCGACCGCGGAGTCCCCGTTCACTGAGGAGACGGA	2160
QY	2161	GACCTGTGACACAGAGCGCTGACAGATGAGAGTCTCCGCTAGAAAGGTTTGGTTG	2220
DB	2161	GACCTGTGACACAGAGCGCTGACAGATGAGAGTCTCCGCTAGAAAGGTTTGGTTG	2220
QY	2221	AAATGCCCGGGGAGCAAACTGACATGGTTGAATGATGATTTCTCTCTGCTTCTC	2280
DB	2221	AAATGCCCGGGGAGCAAACTGACATGGTTGAATGATGATTTCTCTCTGCTTCTC	2280
QY	2281	CTAGATCTGAGCAAGCTGTCTGCTCTCCCGCCCGGAGTATATACATGAGTAACTTTT	2340
DB	2281	CTAGATCTGAGCAAGCTGTCTGCTCTCCCGCCCGGAGTATATACATGAGTAACTTTT	2340
QY	2341	TTAAATTTGTCAAAAGCGCATCTCCAGATTCAGACCTCGCGCATGACTTTTCTGAA	2400
DB	2341	TTAAATTTGTCAAAAGCGCATCTCCAGATTCAGACCTCGCGCATGACTTTTCTGAA	2400
QY	2401	GGTTGCTTTTCCCTCGCCTTTCTGAGGTCGATGAGGAGTCACTGAGGAGTCC	2460
DB	2401	GGTTGCTTTTCCCTCGCCTTTCTGAGGTCGATGAGGAGTCACTGAGGAGTCC	2460
QY	2461	TAACTTTGCACTTTTACTTTTAACTGAACTGAACTTAACTCTCATCCAGCATCTAA	2520
DB	2461	TAACTTTGCACTTTTACTTTTAACTGAACTGAACTTAACTCTCATCCAGCATCTAA	2520
QY	2521	TGCCAGGTTGCTGAGGTAACCTTTTGAAGTAGATATATTACCTGGTCTGTATCTCTTA	2580
DB	2521	TGCCAGGTTGCTGAGGTAACCTTTTGAAGTAGATATATTACCTGGTCTGTATCTCTTA	2580
QY	2581	GTCAATCTCTGGGTACAGGTAATGAGAAATGTAAGTCTTCTCTCCACACCAT	2640
DB	2581	GTCAATCTCTGGGTACAGGTAATGAGAAATGTAAGTCTTCTCTCCACACCAT	2640
QY	2641	ACGATAAAGCAAGACATTTTATAACGATACCGAGTCACTATGCTGCTCTGAAATA	2700
DB	2641	ACGATAAAGCAAGACATTTTATAACGATACCGAGTCACTATGCTGCTCTGAAATA	2700
QY	2701	ACGATTTGAAATCCATGAGTGCAGTATATTTTCTAAAGTTTGGAAAGCAGGTTTTT	2760
DB	2701	ACGATTTGAAATCCATGAGTGCAGTATATTTTCTAAAGTTTGGAAAGCAGGTTTTT	2760
QY	2761	CTTTTAAAGAAATTTAGACACGGTTTCACTAAATGATTTAGTCAAGATTCCTAGACTGA	2820
DB	2761	CTTTTAAAGAAATTTAGACACGGTTTCACTAAATGATTTAGTCAAGATTCCTAGACTGA	2820
QY	2821	AAGAACCTTAAACAAAGAAATTTTAAAGATATAAATATATGCTGATATGTTATGTAAT	2880
DB	2821	AAGAACCTTAAACAAAGAAATTTTAAAGATATAAATATATGCTGATATGTTATGTAAT	2880
QY	2881	TTATTTTAGGCTATAATACATTTTCTTATTTTCCATTTTCAATTAATAATGCTCTAATACA	2940
DB	2881	TTATTTTAGGCTATAATACATTTTCTTATTTTCCATTTTCAATTAATAATGCTCTAATACA	2940
QY	2941	AAAAA	2945


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QY 1021 GAGCAGAGCAACACAGTCAAGGAGCCCAACATCAAGAAATTCACTTGGTGTGATGGC 1080
Db 1021 GAGCAGAGCAACACAGTCAAGGAGCCCAACATCAAGAAATTCACTTGGTGTGATGGC 1080
QY 1081 TCTGTCACTCAGGCTCTGTTTCTGTGATGTTTGGACACCAACGTTGTCTGAGAAAATCTT 1140
Db 1081 TCTGTCACTCAGGCTCTGTTTCTGTGATGTTTGGACACCAACGTTGTCTGAGAAAATCTT 1140
QY 1141 GATAGACATCATCGGAGTGAATTTGCTTTTGAGAACTCTGTGTTGTTTCTTTTGGGAT 1200
Db 1141 GATAGACATCATCGGAGTGAATTTGCTTTTGAGAACTCTGTGTTGTTTCTTTTGGGAT 1200
QY 1201 CTCTCTCTCTCTCCAGTCCAGTCAAGTGAAGGCGCATCTCACGGGTGGCTGATGAC 1260
Db 1201 CTCTCTCTCTCTCCAGTCCAGTCAAGTGAAGGCGCATCTCACGGGTGGCTGATGAC 1260
QY 1261 ACTGAAGAAAACCTTCCTTGTGCGGAGTCTGTGTCGCGGATCATCGTCTCATGCG 1320
Db 1261 ACTGAAGAAAACCTTCCTTGTGCGGAGTCTGTGTCGCGGATCATCGTCTCATGCG 1320
QY 1321 CAGCCTCGTGTCTACCTACCTACCTGCGGTTGACAGTGCAGACCTGGCGGTGGCTCCCT 1380
Db 1321 CAGCCTCGTGTCTACCTACCTACCTGCGGTTGACAGTGCAGACCTGGCGGTGGCTCCCT 1380
QY 1381 CCTGGCGGCTTGTGGGAGAAATCCACATGCTGCGGATCGCTGCTATGTCTACCG 1440
Db 1381 CCTGGCGGCTTGTGGGAGAAATCCACATGCTGCGGATCGCTGCTATGTCTACCG 1440
QY 1441 GAAGCAGAAAAGAGATGAGAAATGAGTGGCCACCGAGGGGGAAGACTCTGCCATGAC 1500
Db 1441 GAAGCAGAAAAGAGATGAGAAATGAGTGGCCACCGAGGGGGAAGACTCTGCCATGAC 1500
QY 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGAAATGAATA 1560
Db 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGAAATGAATA 1560
QY 1561 AGGCAAGGAGCGCCATGGGCACTGAGGAGCGGTGAGTCAAGGATGACACTTCGGCATCAT 1620
Db 1561 AGGCAAGGAGCGCCATGGGCACTGAGGAGCGGTGAGTCAAGGATGACACTTCGGCATCAT 1620
QY 1621 CTCTTCTCTCTCCCTCGATTTGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680
Db 1621 CTCTTCTCTCTCCCTCGATTTGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680
QY 1681 GGCCTTGATTTAAAGGTTTCGTGTCAATTCCTAGCATACCTGGGTATGCTCAACTGACG 1740
Db 1681 GGCCTTGATTTAAAGGTTTCGTGTCAATTCCTAGCATACCTGGGTATGCTCAACTGACG 1740
QY 1741 GGGGACCTAGTGAATGCTTACTGTGCTATGTATGTAAGAAACCAACGAAACAACTGACTT 1800
Db 1741 GGGGACCTAGTGAATGCTTACTGTGCTATGTATGTAAGAAACCAACGAAACAACTGACTT 1800
QY 1801 CATACCCCTGCTCAGCAAAACCCAAAGACACAGCTGCTCAGGTTGAGGTTGTGTCC 1860
Db 1801 CATACCCCTGCTCAGCAAAACCCAAAGACACAGCTGCTCAGGTTGAGGTTGTGTCC 1860
QY 1861 TCCTCCCTGAGCAATCTCTCTTGGAAACCAAGAGCTGAGCTGCGCATCGGCGCTCG 1920
Db 1861 TCCTCCCTGAGCAATCTCTCTTGGAAACCAAGAGCTGAGCTGCGCATCGGCGCTCG 1920
QY 1921 GTACCCCTGACAGAGGCAAGACTCTCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
Db 1921 GTACCCCTGACAGAGGCAAGACTCTCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
QY 1981 CAGGTTAAACTCTCGCTTCTCTTGTATGTTTCCAGTCAACATGGCCGTTCAAGAGATG 2040
Db 1981 CAGGTTAAACTCTCGCTTCTCTTGTATGTTTCCAGTCAACATGGCCGTTCAAGAGATG 2040
QY 2041 GAGCCCGGTGGCTCTTAAATTTCTCTGCGCAGGAGTTCGAAACCACTCTCTCTCAC 2100
Db 2041 GAGCCCGGTGGCTCTTAAATTTCTCTGCGCAGGAGTTCGAAACCACTCTCTCTCAC 2100
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QY 2101 ACATGCGAGGCGGTTGGCAGCTGCGAGCCCGGAGTCCCGTTTCACTGAGGAACGGA 2160
Db 2101 ACATGCGAGGCGGTTGGCAGCTGCGAGCCCGGAGTCCCGTTTCACTGAGGAACGGA 2160
QY 2161 GACCTGTGACACACAGCAGGCTGACAGATGGAACAATCTCCCGTAGAAAGGTTTGGTTG 2220
Db 2161 GACCTGTGACACACAGCAGGCTGACAGATGGAACAATCTCCCGTAGAAAGGTTTGGTTG 2220
QY 2221 AAATGCCCCGGGGCAGCAGAACTGACATGTTGAATGATAGCATTTCACTCTGCGTTCTC 2280
Db 2221 AAATGCCCCGGGGCAGCAGAACTGACATGTTGAATGATAGCATTTCACTCTGCGTTCTC 2280
QY 2281 CTAGATCTGAGCAAGCTCTCAGTTTCTCACCCCCACCGCTGTATATACATGAGCTAACTTT 2340
Db 2281 CTAGATCTGAGCAAGCTCTCAGTTTCTCACCCCCACCGCTGTATATACATGAGCTAACTTT 2340
QY 2341 TTAATTTGTCACAAAGCGCATCTCCAGATTCAGACCCCTGCCGATGACITTTTCTCTGAA 2400
Db 2341 TTAATTTGTCACAAAGCGCATCTCCAGATTCAGACCCCTGCCGATGACITTTTCTCTGAA 2400
QY 2401 GGCCTTGTCTTCCCTCGGCTTCTCTGAAGTTCGCAATAGAGCGAGTCAATGGAGCATCC 2460
Db 2401 GGCCTTGTCTTCCCTCGGCTTCTCTGAAGTTCGCAATAGAGCGAGTCAATGGAGCATCC 2460
QY 2461 TAACTTTGCAATTTAGTTTCTCAGTGAACCTGAAGCTTTAACTCTCATCCAGCATCTCAA 2520
Db 2461 TAACTTTGCAATTTAGTTTCTCAGTGAACCTGAAGCTTTAACTCTCATCCAGCATCTCAA 2520
QY 2521 TGCCAGGTTGCTGAGGTTAACTTTTGAAGTAGATATATACCTGGTTCTGTCTATCTTTA 2580
Db 2521 TGCCAGGTTGCTGAGGTTAACTTTTGAAGTAGATATATACCTGGTTCTGTCTATCTTTA 2580
QY 2581 GTCAATACTCTCGGTACAGGTAATGAGATGTAAGTACTAGGTACTTCCCTCCCAACCAT 2640
Db 2581 GTCAATACTCTCGGTACAGGTAATGAGATGTAAGTACTAGGTACTTCCCTCCCAACCAT 2640
QY 2641 AGGATAAGCAAGACATTTTATAACGATACAGAGTCACTATGTGTCCTCCTCGAAATA 2700
Db 2641 AGGATAAGCAAGACATTTTATAACGATACAGAGTCACTATGTGTCCTCCTCGAAATA 2700
QY 2701 AGGCATTCGAAATCCATGCGAGTCAATTTTCTAAGTTTGGAAAGCAGGTTTCTT 2760
Db 2701 AGGCATTCGAAATCCATGCGAGTCAATTTTCTAAGTTTGGAAAGCAGGTTTCTT 2760
QY 2761 CCTTTAAAGAAATATAGACCGGTTCACTAAATGATTAGTCAAGATTCCTAGACTGA 2820
Db 2761 CCTTTAAAGAAATATAGACCGGTTCACTAAATGATTAGTCAAGATTCCTAGACTGA 2820
QY 2821 AAGAACCTAAACCAAAAAATATTTTAAAGATATAAATATATCTGTATATGTATAT 2880
Db 2821 AAGAACCTAAACCAAAAAATATTTTAAAGATATAAATATATCTGTATATGTATAT 2880
QY 2881 TTAATTTAGGCTATATACATTTCTCTATTTTTCGATTTTCAATAAATGCTCTCTATACA 2940
Db 2881 TTAATTTAGGCTATATATCAATTTCTCTATTTTTCGATTTTCAATAAATGCTCTCTATACA 2940
QY 2941 AAAAA 2945
Db 2941 AAAAA 2945
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RESULT 3

ABK40261

ID ABK40261 standard; cDNA; 2945 BP.

XX AC ABK40261;

XX XX

XX 15-JUL-2002 (first entry)

XX cDNA encoding human PRO274 polypeptide.

XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;

XX leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;

XX

KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX Homo sapiens.
OS WO200153486-A1.
PN XX
PD XX
XX 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US003565.
XX
XX 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ;
PI Marschers SA, Pan J, Picti RM, Roy NA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/36.
DR P-PSDB; AAUS6135.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 50; Fig 15; 302pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX
XX Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;

Query Match 100.0%; Score 2945; DB 6; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCCGCCGTCGCGCCCTCGCTCCGCGAGTCCCTCCGCGGAGAGATGTGTG 60
DB 1 CGTCCCGCCGTCGCGCCCTCGCTCCGCGAGTCCCTCCGCGGAGAGATGTGTG 60
QY 61 GGGTCAGCCACGCGCGGGGACTATGGTGAATTCGCGGCGCTCAGCACTACTGGCCCT 120
DB 61 GGGTCAGCCACGCGCGGGGACTATGGTGAATTCGCGGCGCTCAGCACTACTGGCCCT 120
QY 121 GATCCGGTTCTTGGTGCCTCGGATCACCACATAGGATCGACTTCGGGAGAGGC 180
DB 121 GATCCGGTTCTTGGTGCCTCGGATCACCACATAGGATCGACTTCGGGAGAGGC 180
QY 181 CTTGAACCGGGGCAATTCCTGCTCAAGGAGGATGATCGAGATGCTGCCAGCTACCG 240

DB 181 CTTGAACCGGGGCAATTCCTGCTCAAGGAGGATGATCGAGATGCTGCCAGCTACCG 240
QY 241 GCTGGCGTACTCCCTCATGAAGTTCTTACGGGTCCCATAGTGAATTCAAAAATGTGG 300
DB 241 GCTGGCGTACTCCCTCATGAAGTTCTTACGGGTCCCATAGTGAATTCAAAAATGTGG 300
QY 301 CTTGGTCTTTGTGAACAGCAAGAGAGACAGACGACCAAGCCGCTCTGTATGTGTGGTGGC 360
DB 301 CTTGGTCTTTGTGAACAGCAAGAGAGAGACAGACGACCAAGCCGCTCTGTATGTGTGGTGGC 360
QY 361 AGGGGCCATCGCTGCGCTCTTTCACACATGATAGTATATAGTATTTAGGATACAT 420
DB 361 AGGGGCCATCGCTGCGCTCTTTCACACATGATAGTATATAGTATTTAGGATACAT 420
QY 421 TATCAATAAACTGACCATGTGACGAGTGGTGGGAGCAAGCAGAGAGGCGCTTCCT 480
DB 421 TATCAATAAACTGACCATGTGACGAGTGGTGGGAGCAAGCAGAGAGGCGCTTCCT 480
QY 481 GTACCTCGCGCCCTTTCCTTTCATGACGCAATGGCATGGACCCATGCTGGCATTTCTTT 540
DB 481 GTACCTCGCGCCCTTTCCTTTCATGACGCAATGGCATGGACCCATGCTGGCATTTCTTT 540
QY 541 AAACACAAATACAGTTTCCTGCTGGGATGTCCTCAATCTCAGATGTCATAGCTCAGGT 600
DB 541 AAACACAAATACAGTTTCCTGCTGGGATGTCCTCAATCTCAGATGTCATAGCTCAGGT 600
QY 601 TGTTCCTGTAGCCATTTGCTTTCACAGTACCTGGAATGCCGGAGGCGCTTCATCCC 660
DB 601 TGTTCCTGTAGCCATTTGCTTTCACAGTACCTGGAATGCCGGAGGCGCTTCATCCC 660
QY 661 GATCCTCTCTTGTACATGGCGGACCTTGGCGCTGACACCCCTGCTGGGCTACTA 720
DB 661 GATCCTCTCTTGTACATGGCGGACCTTGGCGCTGACACCCCTGCTGGGCTACTA 720
QY 721 CAAGAACATTCAGACATCATCTCTGACAGAGTGGCCCGGAGCTGGGGGAGATCAAC 780
DB 721 CAAGAACATTCAGACATCATCTCTGACAGAGTGGCCCGGAGCTGGGGGAGATCAAC 780
QY 781 AATGAAGAAATGCTGAGCTTCTGGTGGCCCTTTGGTCTTAATTCCTGGCCACACAGAAAT 840
DB 781 AATGAAGAAATGCTGAGCTTCTGGTGGCCCTTTGGTCTTAATTCCTGGCCACACAGAAAT 840
QY 841 CAGTCCGCTTATTGTCAACCTCTTTGTTCCCGGACCTTGGTGGGAGTCTCAGCCAC 900
DB 841 CAGTCCGCTTATTGTCAACCTCTTTGTTCCCGGACCTTGGTGGGAGTCTCAGCCAC 900
QY 901 AGAGCGAGTGGCGATTTTGAACGACATACCTGTGGGTCAATGCCATACGGCTGGTT 960
DB 901 AGAGCGAGTGGCGATTTTGAACGACATACCTGTGGGTCAATGCCATACGGCTGGTT 960
QY 961 GACGGAATCCGTGCTGTATCTGCTTCGACAAAGATTAACCCAGCAACAACTGGT 1020
DB 961 GACGGAATCCGTGCTGTATCTGCTTCGACAAAGATTAACCCAGCAACAACTGGT 1020
QY 1021 GAGCACAGCAACACAGTACGCGAGCCACATCAAGAAATTCACCTTCCTGTCATGCG 1080
DB 1021 GAGCACAGCAACACAGTACGCGAGCCACATCAAGAAATTCACCTTCCTGTCATGCG 1080
QY 1081 TCTGTCACTACGCTGCTTTCGTTTTCGACACCAACGTCGTCGAGAAATCTT 1140
DB 1081 TCTGTCACTACGCTGCTTTCGTTTTCGACACCAACGTCGTCGAGAAATCTT 1140
QY 1141 GATAGACATCATCGGAGTGGACTTTCCTTTTGAGAACTCTGTGTTTCTTTTGGGAT 1200
DB 1141 GATAGACATCATCGGAGTGGACTTTCCTTTTGAGAACTCTGTGTTTCTTTTGGGAT 1200
QY 1201 CTTTCCTCTTCTCCAGTCCAGTCAAGTGGGCGCATCTCACCGGTGGCTGATGAC 1260
DB 1201 CTTTCCTCTTCTCCAGTCCAGTCAAGTGGGCGCATCTCACCGGTGGCTGATGAC 1260
QY 1261 ACTGAAGAAACCTTCCTTCCTTCGCCCCAGCTCTGTGCTCGGATCATCTCTCTATCGC 1320

Db 1261 ACTGAAGAAAACCTTCGTCTGCCCCCAGCTCTGTCTGGGATCATGTCTCATCGC 1320
Qy 1321 CAGCCTCGTGGTCTACACCTACTCGGGGTGCACGGTGCACACCTGGGGCTGGGCTCCCT 1380
Db 1321 CAGCCTCGTGGTCTACACCTACTCGGGGTGCACGGTGCACACCTGGGGCTGGGCTCCCT 1380
Qy 1381 CCTGGCGGCTTTCTGGGAGAAATCCACATCGTTCGCCATCGCTCGCTGCTATGCTACCG 1440
Db 1381 CCTGGCGGCTTTCTGGGAGAAATCCACATCGTTCGCCATCGCTCGCTGCTATGCTACCG 1440
Qy 1441 GAACAGAAAAGAGATGGAGATGAGTGGCCACCGAGGGGGAAGACTCTGCCATGAC 1500
Db 1441 GAACAGAAAAGAGATGGAGATGAGTGGCCACCGAGGGGGAAGACTCTGCCATGAC 1500
Qy 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGATGAATA 1560
Db 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGATGAATA 1560
Qy 1561 AGGACGGGACGCCATGGGCACTGCAGGACGGTCACTGAGGATGACACTTCGGCATCAT 1620
Db 1561 AGGACGGGACGCCATGGGCACTGCAGGACGGTCACTGAGGATGACACTTCGGCATCAT 1620
Qy 1621 CTCCTTCCTCCCATCGTATTTGTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1680
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Qy 1681 G3CCTTGATTTAAAGTTTCGTCAATTTCTTAGCATCTGCTGAGGATGACACTTCGGCATCAT 1740
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Qy 1741 GGGGACCTAGTGAATGCTTTACTGTTGCTATGTAACCAACCAACCAACCAACCAACCAACCA 1800
Db 1741 GGGGACCTAGTGAATGCTTTACTGTTGCTATGTAACCAACCAACCAACCAACCAACCAACCA 1800
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Qy 1921 GTCACCTGTCAGAGGCCACAGACTCTCTGTCCCCCTTCATCGCTCTTAAGAAACAA 1980
Db 1921 GTCACCTGTCAGAGGCCACAGACTCTCTGTCCCCCTTCATCGCTCTTAAGAAACAA 1980
Qy 1981 CAGGTTAAATCTCGGCTTCCCTTGATTTGCTTCCAGTCAATGCGCGGTACAAAGAGATG 2040
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Db 2161 GACCTGTGACACAGCAGCTGACAGATGGAAGATCTCCGTAGGAAGGTTGGTTG 2220
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Db 2281 CTAGATCTGACAGCTGTGCTGCTCTACCCCCCAGCTGTATATACATGACTTAATTTT 2340
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Qy 2401 G3CCTTGCTTTCCCTCGCTTTCTGAAGTGCATTTAGAGAGTGCATGAGGATCC 2460
Db 2401 G3CCTTGCTTTCCCTCGCTTTCTGAAGTGCATTTAGAGAGTGCATGAGGATCC 2460
Qy 2461 TAACTTTGCATTTTAACTTTTACAGTGAACTGAAGCTTAAAGTCTCATCCAGCATTTCAA 2520
Db 2461 TAACTTTGCATTTTAACTTTTACAGTGAACTGAAGCTTAAAGTCTCATCCAGCATTTCAA 2520
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Db 2521 TCCAGGTTGCTGTAGGTTAACTTTTGAAGTAGATATATTACCTGCTTCTGATCCCTTA 2580
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Qy 2881 TTAATTTAGGCTATTAATACATTTCCCTATTTTCGCAATTTTCAATAAATGCTCTTAATACA 2940
Db 2881 TTAATTTAGGCTATTAATACATTTCCCTATTTTCGCAATTTTCAATAAATGCTCTTAATACA 2940
Qy 2941 AAAAA 2945
Db 2941 AAAAA 2945

RESULT 4
ACD42428
ID ACD42428 standard; cDNA; 2945 BP.
XX ACD42428;
XX
XX
XX 09-SEP-2003 (first entry)
XX
XX
XX Novel human secreted and transmembrane protein PRO274 cDNA.
XX Human, secreted and transmembrane protein; PRO; virucide; gene therapy;
XX cell death; growth induction cascade; blood coagulation cascade;
XX viral infection; gene; ss.
XX Homo sapiens.
XX
XX US2003050239-A1.
XX
XX
XX 13-MAR-2003.
XX
XX 15-OCT-2001; 2001US-00978191.
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XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.

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PR	20-MAR-1998;	98US-0078936P.	PR	22-MAY-1998;	98US-0086430P.
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PR	27-MAR-1998;	98US-0079689P.	PR	28-JUN-1998;	98US-0090863P.
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PR	30-MAR-1998;	98US-0079920P.	PR	01-JUL-1998;	98US-0091359P.
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PR	31-MAR-1998;	98US-0080194P.	PR	02-NOV-1998;	98US-00184216.
PR	01-APR-1998;	98US-0080327P.	PR	06-NOV-1998;	98US-00187368.
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PR	15-APR-1998;	98US-0081817P.	PR	10-MAR-1999;	98US-00265686.
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PR	22-APR-1998;	98US-0082700P.	PR	28-APR-1999;	98US-0131445P.
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PR	23-APR-1998;	98US-0083336P.	PR	16-JUN-1999;	98US-0139557P.
PR	28-APR-1998;	98US-0083322P.	PR	23-JUN-1999;	98US-0141037P.
PR	28-APR-1998;	98US-0083392P.	PR	07-JUL-1999;	98US-0142680P.
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PR	05-MAY-1998;	98US-0084366P.	PR	30-DEC-1999;	98US-00311243.
PR	06-MAY-1998;	98US-0084414P.	PR	30-DEC-1999;	98US-00311274.
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PR	07-MAY-1998;	98US-0084627P.	PR	06-JAN-2000;	2000US-0000376.
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PR	13-MAY-1998;	98US-0085338P.	PR	10-MAR-2000;	2000US-0006319.
PR	13-MAY-1998;	98US-0085339P.	PR	21-MAR-2000;	2000US-0007532.
PR	15-MAY-1998;	98US-0085573P.	PR	30-MAR-2000;	2000US-0008439.
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PR	15-MAY-1998;	98US-0085700P.	PR	24-AUG-2000;	2000US-0023238.
PR	15-MAY-1998;	98US-0085700P.	PR	08-NOV-2000;	2000US-00709238.

09-APR-1998; 98US-0081195P.
09-APR-1998; 98US-0081203P.
09-APR-1998; 98US-0081229P.
15-APR-1998; 98US-0081817P.
15-APR-1998; 98US-0081819P.
15-APR-1998; 98US-0081838P.
15-APR-1998; 98US-0081952P.
15-APR-1998; 98US-0081955P.
21-APR-1998; 98US-0082568P.
21-APR-1998; 98US-0082569P.
22-APR-1998; 98US-0082700P.
22-APR-1998; 98US-0082704P.
22-APR-1998; 98US-0082797P.
22-APR-1998; 98US-0082804P.
23-APR-1998; 98US-0082796P.
07-OCT-1998; 98WO-US021141.
20-NOV-1998; 98WO-US021485.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
10-MAR-1999; 99WO-US005190.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
03-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
08-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001WO-US009552.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019592.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
(GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-328860/31.
DR P-PSDB; ABU72194.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
XX Claim 2; Fig 3; 453pp; English.
PS
XX The invention describes an isolated nucleic acid (I) comprising, or which

CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;
Query Match 100.0%; Score 2945; DB 7; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCTCGCCCGTGGCCCTCCCGCCAGAGTCCCTCGCGGAGCAGAGTGTGTG 60
DB 1 CGCTCGCCCGTGGCCCTCCCGCCAGAGTCCCTCGCGGAGCAGAGTGTGTG 60
QY 61 GGTCAGCCACCGCGGGGACTATGTGAAATTCGCGGCTCAGCACTACTGCCCT 120
DB 61 GGTCAGCCACCGCGGGGACTATGTGAAATTCGCGGCTCAGCACTACTGCCCT 120
QY 121 GATCGGTTCTTGGTGGCCCTGGGCATCAACCAATAGCCATCTCGGGGAGCAGG 180
DB 121 GATCGGTTCTTGGTGGCCCTGGGCATCAACCAATAGCCATCTCGGGGAGCAGG 180
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DB 181 CTTGAACCGGGGATTCGCTGCTGCAAGGAGGATCGAGATGCTGGCAGTACGG 240
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DB 481 GTACCTCGCGGCTTTTCTTTCATGAGCAATGCGACCCCATGCTGGCATTTCT 540
QY 541 AAAACACAAATACAGTTTCTGGTGGGATGTCCTCAATCTCAGATGCTAGTCAAGT 600
DB 541 AAAACACAAATACAGTTTCTGGTGGGATGTCCTCAATCTCAGATGCTAGTCAAGT 600
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DB 601 TGTGTTTGTAGCCATTTTCTTTCAGTCACTGCAAGTCCGAGGAGCCCTGCTCATCC 660
QY 661 GATCTCTCTCTTGTATACATGGGCGCACTTGTGGCTGACACCCCTGTGCTGGGTACT 720
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QY 721 CAAGAACATTCAGCATCATCCCTGACAGAGTGGCCGAGCTGGGGGAGATGCAAC 780
DB 721 CAAGAACATTCAGCATCATCCCTGACAGAGTGGCCGAGCTGGGGGAGATGCAAC 780
QY 781 AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAATTTCTGGCCACACAGAGAT 840
DB 781 AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAATTTCTGGCCACACAGAGAT 840

CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide

781	ATATAGAAAGATGCTGAGCTTCTGGTGGCCCTTTGGCTCTTAATTTCTGCCACACAGAGAA	840
Qy	CAGTCGCCCTATTGTCTCAACCTCTTTGTTTCCCGGACCTTTGGTGGCAGTTTCTGCAGCCAC	900
Db	CAGTCGCCCTATTGTCAACCTCTTTGTTTCCCGGACCTTTGGTGGCAGTTTCTGCAGCCAC	900
Qy	AGAGGCAGTCGGCAGTTTTCAGGCCACATACCCTGTGGGTTCACATCCCATACCGCTGGTT	960
Db	AGAGGCAGTCGGCAGTTTTCAGGCCACATACCCTGTGGGTTCACATCCCATACCGCTGGTT	960
Qy	GACGGAAATCCGTGCTGTGTATCTGTTTCGACAGAATAAACCCGACCAACAACTGGT	1020
Db	GACGGAAATCCGTGCTGTGTATCTGTTTCGACAGAATAAACCCGACCAACAACTGGT	1020
Qy	GAGCACAGCAACACAGTTCAGCGGACGCCACATCAAGAAGTTCACTTGTCTGCAATGCC	1080
Db	GAGCACAGCAACACAGTTCAGCGGACGCCACATCAAGAAGTTCACTTGTCTGCAATGCC	1080
Qy	TCTGTCTACACGCTCTGTTTTCAGGATGTTTTTGGACACCCAACTGTCTGAGAAAATCTT	1140
Db	TCTGTCTACACGCTCTGTTTTCAGGATGTTTTTGGACACCCAACTGTCTGAGAAAATCTT	1140
Qy	GATAGACATCATCGAGTGGACTTTGCTTTTGAGAACTCTGTGTGTTCTTTGGGAT	1200
Db	GATAGACATCATCGAGTGGACTTTGCTTTTGAGAACTCTGTGTGTTCTTTGGGAT	1200
Qy	CTTCTCTCTTTCCAGTTTCAGTTCACAGTGAAGGCGGCATCTCACGGGTGGCTGATGAC	1260
Db	CTTCTCTCTTTCCAGTTTCAGTTCACAGTGAAGGCGGCATCTCACGGGTGGCTGATGAC	1260
Qy	ACTGAAGAAAACCTTCGTCCTTGGCCCCAGCTCTGTGCTGGATCATCTGCTCTCATCGC	1320
Db	ACTGAAGAAAACCTTCGTCCTTGGCCCCAGCTCTGTGCTGGATCATCTGCTCTCATCGC	1320
Qy	CAGCCTGTGGTCTTACCTACTTGGGGGTGCACGGTGCACCTCGGGCGTGGGCTCCCT	1380
Db	CAGCCTGTGGTCTTACCTACTTGGGGGTGCACGGTGCACCTCGGGCGTGGGCTCCCT	1380
Qy	CCTGGCGGGCTTTGTGGAGAAATCCACCATGGTGCCTATCGCTCGCTGCTATGTCTACCG	1440
Db	CCTGGCGGGCTTTGTGGAGAAATCCACCATGGTGCCTATCGCTCGCTGCTATGTCTACCG	1440
Qy	GRAGCAGAAAGAGATGGAGATGAGTCGGCCACGGAGGGGAGACTCTGCCATGAC	1500
Db	GAAGCAGAAAGAGATGGAGATGAGTCGGCCACGGAGGGGAGACTCTGCCATGAC	1500
Qy	AGACATGCTCCGACAGAGGAGTGCAGACATCGTGGAAATGAGAGAGAGAAATGAATA	1560
Db	AGACATGCTCCGACAGAGGAGTGCAGACATCGTGGAAATGAGAGAGAGAAATGAATA	1560
Qy	AGGCACGGAGCCCATGGCACTTCAGGACGGTCACTCAGGATGACATTCGGCATCAT	1620
Db	AGGCACGGAGCCCATGGCACTTCAGGACGGTCACTCAGGATGACATTCGGCATCAT	1620
Qy	CTCTTCCCTCTCCCATCGTATTTGTTCCTTTTTTTGTTTTGTTGTAATGAAAGA	1680
Db	CTCTTCCCTCTCCCATCGTATTTGTTCCTTTTTTTGTTTTGTTGTAATGAAAGA	1680
Qy	GGCCTTCGATTTAAAGTTTCGTGTCAATCTCTAGCATATCTGGGTATGCTCACATGACG	1740
Db	GGCCTTCGATTTAAAGTTTCGTGTCAATCTCTAGCATATCTGGGTATGCTCACATGACG	1740
Qy	GGGGGACCTAGTGAATGGTCTTTACTGTGTATGTATGTAAAAACAAACAACTGACTT	1800
Db	GGGGGACCTAGTGAATGGTCTTTACTGTGTATGTATGTAAAAACAAACAACTGACTT	1800
Qy	CATACCCTGCCTCAGGAAACCCAAAGACACAGCTGCCTCAGGTGTGAGTTGTGTCC	1860
Db	CATACCCTGCCTCAGGAAACCCAAAGACACAGCTGCCTCAGGTGTGAGTTGTGTCC	1860
Qy	TCCTTCCCTGGACAATCTCTCTTTGGAACCAAGGACTGACGTGTGCCATCGCGCTCG	1920
Db	TCCTTCCCTGGACAATCTCTCTTTGGAACCAAGGACTGACGTGTGCCATCGCGCTCG	1920

Qy	1921	GTCA	CCCTGTGCA	CAGAGGCCACAGACTCTCTGTCCTCCCTTCATCGCTCTTAA	GAACTCAA	1980
Db	1921	GTCA	CCCTGTGCA	CAGAGGCCACAGACTCTCTGTCCTCCCTTCATCGCTCTTAA	GAACTCAA	1980
Qy	1981	CAGG	TTAAAACTCGGCTTCCTTTG	TAATTCCTCCAGTCACATGCGCGGTACAAAGAGATG		2040
Db	1981	CAGG	TTAAAACTCGGCTTCCTTTG	TAATTCCTCCAGTCACATGCGCGGTACAAAGAGATG		2040
Qy	2041	GAGC	CCCGGTGGCTCTTAAATTC	CCCTCTGCGACGAGATTCGAAACCATCTACTCCAC		2100
Db	2041	GAGC	CCCGGTGGCTCTTAAATTC	CCCTCTGCGACGAGATTCGAAACCATCTACTCCAC		2100
Qy	2101	ACAT	GACGAGAGCGCGGTGGCGAC	CGCTGGAGCCCGGAGTCCTCCCTTCACATGAGGAAACGGA		2160
Db	2101	ACAT	GACGAGAGCGCGGTGGCGAC	CGCTGGAGCCCGGAGTCCTCCCTTCACATGAGGAAACGGA		2160
Qy	2161	GACCT	GTGACACACAGCAGCGCTG	ACAGATGGACAGAAATCTCCCGTGAAGAGTTTGGTTTG		2220
Db	2161	GACCT	GTGACACACAGCAGCGCTG	ACAGATGGACAGAAATCTCCCGTGAAGAGTTTGGTTTG		2220
Qy	2221	AAAT	GCCCCGGGGCAGCAACATG	ACATGATGTTGCAATAGACATTTCACTCTGGGTCTC		2280
Db	2221	AAAT	GCCCCGGGGCAGCAACATG	ACATGATGTTGCAATAGACATTTCACTCTGGGTCTC		2280
Qy	2281	CTAG	ATCTGAGCAGACTGTCTAG	TTCTCACCCCCACCGTGTATATACATGAGCTAACTTTT		2340
Db	2281	CTAG	ATCTGAGCAGACTGTCTAG	TTCTCACCCCCACCGTGTATATACATGAGCTAACTTTT		2340
Qy	2341	TTAA	TTGTGCAAAAGCGCATCTCC	AGATTCACAGACCCTGCCGATGACATTTTCTGAA		2400
Db	2341	TTAA	TTGTGCAAAAGCGCATCTCC	AGATTCACAGACCCTGCCGATGACATTTTCTGAA		2400
Qy	2401	GGCT	TCCTTCCCTCGGCTTCTG	AGGTCGCATTAGCGGAGTCACATGGAGCATCC		2460
Db	2401	GGCT	TCCTTCCCTCGGCTTCTG	AGGTCGCATTAGCGGAGTCACATGGAGCATCC		2460
Qy	2461	TAA	CTTTGCATTTAGTTTTPAC	AGTGAATGAAGCTTTAAGTCTCATCCAGCATCTCAA		2520
Db	2461	TAA	CTTTGCATTTAGTTTTPAC	AGTGAATGAAGCTTTAAGTCTCATCCAGCATCTCAA		2520
Qy	2521	TGCG	AGGTGCTGTAGGGTAACTTT	TGCAAGTACATATATTACCTGGTCTGCTATCCCTTA		2580
Db	2521	TGCG	AGGTGCTGTAGGGTAACTTT	TGCAAGTACATATATTACCTGGTCTGCTATCCCTTA		2580
Qy	2581	GTCA	TAACTCTGCGGTACAGGTAA	TTGAGAAATGTCTACGGTACTTCCCTGCCACACCAT		2640
Db	2581	GTCA	TAACTCTGCGGTACAGGTAA	TTGAGAAATGTCTACGGTACTTCCCTGCCACACCAT		2640
Qy	2641	ACGA	TAAACAGACATTTTATA	ACGATACACAGAGTCATGTGGTCTCCCTCGAATA		2700
Db	2641	ACGA	TAAACAGACATTTTATA	ACGATACACAGAGTCATGTGGTCTCCCTCGAATA		2700
Qy	2701	ACGC	ATTGGAATCCATGCGAGT	GCAGTATATTTTCTTAAGTTTTCGAAAGCAGGTTTTTT		2760
Db	2701	ACGC	ATTGGAATCCATGCGAGT	GCAGTATATTTTCTTAAGTTTTCGAAAGCAGGTTTTTT		2760
Qy	2761	CCTT	TTAAAAAATATAGACAGG	TTCACTAAATTCGATTTAGTCAGAAATTCCTAGACATGA		2820
Db	2761	CCTT	TTAAAAAATATAGACAGG	TTCACTAAATTCGATTTAGTCAGAAATTCCTAGACATGA		2820
Qy	2821	AAGA	CCCTAAACAAAAAATATTTT	TAAAGATATAAAATATATGCTGTATATGTATTGTAAT		2880
Db	2821	AAGA	CCCTAAACAAAAAATATTTT	TAAAGATATAAAATATATGCTGTATATGTATTGTAAT		2880
Qy	2881	TTAT	TTTATAGGCTTAATACATTT	CTCTATTTTCGCATTTTCAATAAATGCTCTTAATACA		2940
Db	2881	TTAT	TTTATAGGCTTAATACATTT	CTCTATTTTCGCATTTTCAATAAATGCTCTTAATACA		2940
Qy	2941	AAAA			2945	
Db	2941	AAAA			2945	

RESULT 6
ACA71627
ACA71627 standard; cDNA; 2945 BP.
ACA71627;
11-AUG-2003 (first entry)
Human secreted and transmembrane polypeptide PRO274 cDNA.
Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine; erythropoietin; colony stimulating factor; cancer; colorectal carcinoma; apoptosis related condition; AIDS; amyotrophic lateral sclerosis; inflammatory disease; asthma; atherosclerosis; neurodegenerative disease; gastrointestinal disorder; Alzheimer's disease; Parkinson's disease; hypertension; myocardial ischaemia; kidney disease; carcinogenesis; glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia; bronchial asthma; gastric ulcer; renal failure; cardiovascular disease; inflammatory bowel disease; reproductive disorder; premature labour.
Homo sapiens.
US2002177553-A1.
28-NOV-2002.
15-OCT-2001; 2001US-00978192.
17-OCT-1997; 97US-00622250P.
03-NOV-1997; 97US-0064249P.
13-NOV-1997; 97US-0065311P.
21-NOV-1997; 97US-0065364P.
10-MAR-1998; 98US-0077450P.
11-MAR-1998; 98US-0077632P.
11-MAR-1998; 98US-0077641P.
12-MAR-1998; 98US-0077791P.
13-MAR-1998; 98US-0078004P.
17-MAR-1998; 98US-0040220P.
20-MAR-1998; 98US-0078886P.
20-MAR-1998; 98US-0078910P.
20-MAR-1998; 98US-0078936P.
20-MAR-1998; 98US-0078939P.
25-MAR-1998; 98US-0079294P.
26-MAR-1998; 98US-0079656P.
27-MAR-1998; 98US-0079663P.
27-MAR-1998; 98US-0079664P.
27-MAR-1998; 98US-0079689P.
27-MAR-1998; 98US-0079728P.
27-MAR-1998; 98US-0079786P.
30-MAR-1998; 98US-0079920P.
30-MAR-1998; 98US-0079923P.
26-JUN-1998; 98US-00105413.
07-OCT-1998; 98US-00168978.
07-OCT-1998; 98WO-US021141.
02-NOV-1998; 98US-00184216.
06-NOV-1998; 98US-00187368.
20-NOV-1998; 98WO-US024855.
07-DEC-1998; 98US-00202054.
22-DEC-1998; 98US-00218517.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99US-00254465.
08-MAR-1999; 99WO-US005028.
10-MAR-1999; 99US-00265686.
10-MAR-1999; 99WO-US005190.
12-MAR-1999; 99US-00267213.
12-APR-1999; 99US-00284291.
14-MAY-1999; 99US-00311832.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
25-AUG-1999; 99US-00380137.
25-AUG-1999; 99US-00380138.


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QY 1921 GTCACTCTGACAGCAGGCGACAGACTCTCTGTGTCCTCCCTTCAATCGCTTTAAGAATCAA 1980
Db 1921 GTCACTCTGACAGCAGGCGACAGACTCTCTGTGTCCTCCCTTCAATCGCTTTAAGAATCAA 1980
QY 1981 CAGGTTAAACTCGGCTTCTTTGATTTGTTTCCCAAGTCACATGGCGGTACAAAGAGATG 2040
Db 1981 CAGGTTAAACTCGGCTTCTTTGATTTGTTTCCCAAGTCACATGGCGGTACAAAGAGATG 2040
QY 2041 GAGCCCGGTGGCTCTTAAATTCCTTTCTGACCGAGTTCGAAACCATCTACTCCAC 2100
Db 2041 GAGCCCGGTGGCTCTTAAATTCCTTTCTGACCGAGTTCGAAACCATCTACTCCAC 2100
QY 2101 ACATGACGAGGCGGTGGCGCTGACCGCTGACCGGAGTCCCGTTCACATGAGGAGCGA 2160
Db 2101 ACATGACGAGGCGGTGGCGCTGACCGCTGACCGGAGTCCCGTTCACATGAGGAGCGA 2160
QY 2161 GACCTGTGACACAGCAGGCTGACAGATGACAGATCTCCCGTAGAAAGGTTTGGTTTG 2220
Db 2161 GACCTGTGACACAGCAGGCTGACAGATGACAGATCTCCCGTAGAAAGGTTTGGTTTG 2220
QY 2221 AATGTCGCGGGGCGACAACTGACATGGTTGAATGATAGCTTTCACTCTCGGTTCTC 2280
Db 2221 AATGTCGCGGGGCGACAACTGACATGGTTGAATGATAGCTTTCACTCTCGGTTCTC 2280
QY 2281 CTAGATCTGAGCAAGCTGTCTCAGTTCTCACCCCGCTGTATATACATGAGCTAACTTTT 2340
Db 2281 CTAGATCTGAGCAAGCTGTCTCAGTTCTCACCCCGCTGTATATACATGAGCTAACTTTT 2340
QY 2341 TTAATGTCACAAAGCGCATCTCAGATTCAGACCTCGCGCATGACTTTCTCTGAA 2400
Db 2341 TTAATGTCACAAAGCGCATCTCAGATTCAGACCTCGCGCATGACTTTCTCTGAA 2400
QY 2401 GGCTTGCTTTTCCCTGCTCTTCTGAGGTGCGATTTAGAGCGAGTCAATGGAGCATCC 2460
Db 2401 GGCTTGCTTTTCCCTGCTCTTCTGAGGTGCGATTTAGAGCGAGTCAATGGAGCATCC 2460
QY 2461 TAATTTGCAATTTAGTTTTCAGTGAATGAGTCTTAAGTCTCATCGAGCATCTAA 2520
Db 2461 TAATTTGCAATTTAGTTTTCAGTGAATGAGTCTTAAGTCTCATCGAGCATCTAA 2520
QY 2521 TGCAGGTTCTGCTAGGTAATTTTGAAGTAGATATATTACCTGTTCTGCTATCCTTA 2580
Db 2521 TGCAGGTTCTGCTAGGTAATTTTGAAGTAGATATATTACCTGTTCTGCTATCCTTA 2580
QY 2581 GTCATAACTCTGCGGTACAGGTAATTGAGAAATGTAAGTCTTCCCTCCACACCAT 2640
Db 2581 GTCATAACTCTGCGGTACAGGTAATTGAGAAATGTAAGTCTTCCCTCCACACCAT 2640
QY 2641 ACGATAAGCAGACATTTTATAACGATACAGAGTCACATGCTGCTCCCTGGAATA 2700
Db 2641 ACGATAAGCAGACATTTTATAACGATACAGAGTCACATGCTGCTCCCTGGAATA 2700
QY 2701 ACGCATTCGAAATCCATGCGAGTCAGTATATTTTCTAACTTTTGAAGCAGGTTTIT 2760
Db 2701 ACGCATTCGAAATCCATGCGAGTCAGTATATTTTCTAACTTTTGAAGCAGGTTTIT 2760
QY 2761 CTTTAAATAAATATATAGACAGGTTCAATAATGATTTAGTCAGAAATTCCTAGACTGA 2820
Db 2761 CTTTAAATAAATATATAGACAGGTTCAATAATGATTTAGTCAGAAATTCCTAGACTGA 2820
QY 2821 AAGAACCTTAAACAAAAAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAAT 2880
Db 2821 AAGAACCTTAAACAAAAAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAAT 2880
QY 2881 TTATTTAGGCTAATAATACATTTCTCTATTTTCGCAATTTTCAATAAATGCTCTAATACA 2940
Db 2881 TTATTTAGGCTAATAATACATTTCTCTATTTTCGCAATTTTCAATAAATGCTCTAATACA 2940
QY 2941 AAAAA 2945
Db 2941 AAAAA 2945
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RESULT 7
ABX92267
ID ABX92267 standard; cDNA; 2945 BP.
XX
AC ABX92267;
XX
DT 08-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO274 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
KW cardiant; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-00978697.
XX
PR 26-MAY-1981; 81US-00267213.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0085311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187358.
PR 20-NOV-1998; 98US-0024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-0000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99US-0005028.
PR 10-MAR-1999; 99US-00265656.
PR 12-MAR-1999; 99US-0005190.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00310733.
PR 02-JUN-1999; 99US-0012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-0028313.
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PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 05-DEC-1999; 99WO-US031274.
 PR 30-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000US-00709238.
 PR 27-NOV-2000; 2000US-00723749.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00816920.
 PR 22-MAR-2001; 2001WO-US009552.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00854280.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-288163/28.
 DR P-PSDB; ABU61072.
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies.
 XX
 PS Claim 2; Fig 3; 459pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The bioactive molecule may be a
 CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
 CC The PRO polypeptides are useful for treating immune disorders, diabetes
 CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
 CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
 CC tumours, and wound healing. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and gene

CC mapping, in the generation of antisense RNA and DNA, in the preparation
 CC of PRO polypeptides, for generating transgenic animals or knockout
 CC animals, for the genetic analysis of individuals with genetic disorders,
 CC and in gene therapy. The present sequence encodes a human PRO polypeptide
 CC of the invention. Note: The sequence data for this patent was obtained in
 CC electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsIDentry.html
 XX
 SQ Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2945; DB 7; Length 2945;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCTGCCCGCTCGCCCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60
 DB 1 CGCTGCCCGCTCGCCCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60
 QY 61 GGGTCAGCCACCGCGGGGACTATGTTGAAATTCGCCGGCTCAGCCTACTG 120
 DB 61 GGGTCAGCCACCGCGGGGACTATGTTGAAATTCGCCGGCTCAGCCTACTG 120
 QY 121 GATCCGGTTCCTGGTGGCCCTCGGCATCACCACATAGCCATCGCTTCGGG 180
 DB 121 GATCCGGTTCCTGGTGGCCCTCGGCATCACCACATAGCCATCGCTTCGGG 180
 QY 181 CTTGAACCGGGGCAATGTCTGTCAAGGAGATGCGATCGAGATGCTGGCC 240
 DB 181 CTTGAACCGGGGCAATGTCTGTCAAGGAGATGCGATCGAGATGCTGGCC 240
 QY 241 GCTGGGTAATCCCTCATGAAGTTCCTCAGCGGTCCCATGAGTCTCAAAA 300
 DB 241 GCTGGGTAATCCCTCATGAAGTTCCTCAGCGGTCCCATGAGTCTCAAAA 300
 QY 301 CTTGGTGTGTTGAACAGCAGAGACAGGACCAAGCCGCTCTGTGTATG 360
 DB 301 CTTGGTGTGTTGAACAGCAGAGACAGGACCAAGCCGCTCTGTGTATG 360
 QY 361 AGGGGCAATCGCTGGCTCTTTCACACATGATGATGATTTAGGATACAT 420
 DB 361 AGGGGCAATCGCTGGCTCTTTCACACATGATGATGATTTAGGATACAT 420
 QY 421 TATCAATAAATGCACTGACCATGTGACGATCGGTGGGAGCAAGAGAGG 480
 DB 421 TATCAATAAATGCACTGACCATGTGACGATCGGTGGGAGCAAGAGAGG 480
 QY 481 GTACCTGGCGCTCTTTCCTTTCATGAGCAATGCGATGCAATGCTGGCAT 540
 DB 481 GTACCTGGCGCTCTTTCCTTTCATGAGCAATGCGATGCAATGCTGGCAT 540
 QY 541 AAAACACAAATACAGTTTCTCTGTTGGTGTGCTCAATCTCAGATGTCT 600
 DB 541 AAAACACAAATACAGTTTCTCTGTTGGTGTGCTCAATCTCAGATGTCT 600
 QY 601 TGTGTTGTAGCCATTTGCTTTCACAGTCACTGGAAATCCGGGAGCCCTG 660
 DB 601 TGTGTTGTAGCCATTTGCTTTCACAGTCACTGGAAATCCGGGAGCCCTG 660
 QY 661 GATCCTCTCTGTTGATGAGGCGCCTGTGCGCTGCACACCCCTGTGCT 720
 DB 661 GATCCTCTCTGTTGATGAGGCGCCTGTGCGCTGCACACCCCTGTGCT 720
 QY 721 CAAGAACATTCAGACATCATCTCTGACAGAGTGGCCCGGAGCTGGGG 780
 DB 721 CAAGAACATTCAGACATCATCTCTGACAGAGTGGCCCGGAGCTGGGG 780
 QY 781 AATGAAGAAGATGCTGAGCTTCTGTTGGCTTTGGCTCTAATTTCTGG 840
 DB 781 AATGAAGAAGATGCTGAGCTTCTGTTGGCTTTGGCTCTAATTTCTGG 840
 QY 841 CAGTGGCGCTATTGTTCAACCTCTTTGTTTCCCGGGACCTTTGGTGG 900
 DB 841 CAGTGGCGCTATTGTTCAACCTCTTTGTTTCCCGGGACCTTTGGTGG 900

901 AGAGCAGTGGCGATTTTGACAGCCACATACCCCTGTGGGTACATGCCATACGGCTGGTT 960
901 AGAGCAGTGGCGATTTTGACAGCCACATACCCCTGTGGGTACATGCCATACGGCTGGTT 960
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1021 GAGCAGAGCAACACAGTCAAGAGCCACATCAAGAAATTAACCCAGCAACAACCTGGT 1080
1021 GAGCAGAGCAACACAGTCAAGAGCCACATCAAGAAATTAACCCAGCAACAACCTGGT 1080
1081 TCTGTCACTCAAGCTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
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1141 GATAGACATCATCGAGTGGATTTTGGCTTTGCGAATCTGTGTGTGTGTGTGTGTGTGTGTGT 1200
1141 GATAGACATCATCGAGTGGATTTTGGCTTTGCGAATCTGTGTGTGTGTGTGTGTGTGTGTGT 1200
1201 CTTCTCCTTCTCCAGTTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 1260
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1381 CTTGCGGGCTTTGTTGGGAGATCCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
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1441 GAAAGCAAAAAGAGATGGAGATGAGTCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
1501 AGACATGCTCCGACAGAGAGGAGTACAGACATCGTGAAATGAGAGAGGAGGAGGAGGAGGAG 1560
1501 AGACATGCTCCGACAGAGAGGAGTACAGACATCGTGAAATGAGAGAGGAGGAGGAGGAGGAG 1560
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1561 AGCAGCGGACGCGCATGGGCACTGCGAGGAGGAGTACAGGATGAGGATGAGGATGAGGATGAG 1620
1621 CTTCTCCCTCTCCATCGTATTTGTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680
1621 CTTCTCCCTCTCCATCGTATTTGTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680
1681 GGCCTTTGATTTAAAGTTTGTGTCAATTTCTCTAGCATCTGCGTATGCTCACTGAGCG 1740
1681 GGCCTTTGATTTAAAGTTTGTGTCAATTTCTCTAGCATCTGCGTATGCTCACTGAGCG 1740
1741 GGGGACCTAGTGAATGGTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1741 GGGGACCTAGTGAATGGTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1801 CATAACCTCCCTCAGCAAAACCCAAAGACACAGCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCT 1860
1801 CATAACCTCCCTCAGCAAAACCCAAAGACACAGCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCT 1860
1861 TCTCTCCCTGGCAATCTCTCTGGAACCAAGAGGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1861 TCTCTCCCTGGCAATCTCTCTGGAACCAAGAGGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1921 GTCAACCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
1921 GTCAACCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980

RESULT 8
ACA66008
ID ACA66008 standard; cDNA; 2945 BP.
XX

1981 CAGGTTAAACCTCGGCTTCCCTTTGATTTGCTTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 2040
1981 CAGGTTAAACCTCGGCTTCCCTTTGATTTGCTTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 2040
2041 GAGCCCCGCTGGCTCTTAAATTTCCCTTCTGCCACGGAGTTCCGAAACCATCTACTCCAC 2100
2041 GAGCCCCGCTGGCTCTTAAATTTCCCTTCTGCCACGGAGTTCCGAAACCATCTACTCCAC 2100
2101 ACATGACAGAGGCGGCTGGCAGCTGACGCTGCCGAGTCCCGGTTCCACATCTGAGGAAACGGA 2160
2101 ACATGACAGAGGCGGCTGGCAGCTGACGCTGCCGAGTCCCGGTTCCACATCTGAGGAAACGGA 2160
2161 GACCTGTGACCAACAGCAGGCTGACAGATGAGAGATCTCCCGTAGAAGAGTTGGTTTG 2220
2161 GACCTGTGACCAACAGCAGGCTGACAGATGAGAGATCTCCCGTAGAAGAGTTGGTTTG 2220
2221 AATGCCCCGGGGGAGCAAACTGACATGGTGAATGATAGATTTCACTCTGCGTTCTC 2280
2221 AATGCCCCGGGGGAGCAAACTGACATGGTGAATGATAGATTTCACTCTGCGTTCTC 2280
2281 CTAGATCTGAGCAAGCTGTCAAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTT 2340
2281 CTAGATCTGAGCAAGCTGTCAAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTT 2340
2341 TTAATTTGTACAAAAGCGCATCTCCAGATTCAGACCTCCGCGCATGACTTTTCTCTGAA 2400
2341 TTAATTTGTACAAAAGCGCATCTCCAGATTCAGACCTCCGCGCATGACTTTTCTCTGAA 2400
2401 GGCTTGCTTTTCCCTCGCCTTTCTCGAAGTCCATTTAGAGCGAGTCCATGAGGAGTCC 2460
2401 GGCTTGCTTTTCCCTCGCCTTTCTCGAAGTCCATTTAGAGCGAGTCCATGAGGAGTCC 2460
2461 TTAATTTGTACAAAAGCGCATCTCCAGTGAAGCTTTAAGTCTCATCCAGCATTTCTAA 2520
2461 TTAATTTGTACAAAAGCGCATCTCCAGTGAAGCTTTAAGTCTCATCCAGCATTTCTAA 2520
2521 TGCAGAGTCTGTAGGTAACCTTTTGAAGTAGATATATTTACCTGGTTCTGCTATCTTTA 2580
2521 TGCAGAGTCTGTAGGTAACCTTTTGAAGTAGATATATTTACCTGGTTCTGCTATCTTTA 2580
2581 GTCTATACTCTGCGGTACAGGTAATTGAGAAATGCTACTACGTTACTTCCCTCCACACCAT 2640
2581 GTCTATACTCTGCGGTACAGGTAATTGAGAAATGCTACTACGTTACTTCCCTCCACACCAT 2640
2641 ACATTAAGCAAGACATTTTATAACGATACAGAGTCACTATGTGTGTCTCTCCCTGAAATA 2700
2641 ACATTAAGCAAGACATTTTATAACGATACAGAGTCACTATGTGTGTCTCTCCCTGAAATA 2700
2701 ACGCATTCGAAATCCATGCGAGTGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTT 2760
2701 ACGCATTCGAAATCCATGCGAGTGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTT 2760
2761 CTTTAAAGAAATTTATAGACAGCTTCACTAAATTTAGTCAAGATTTCTTAGACTGA 2820
2761 CTTTAAAGAAATTTATAGACAGCTTCACTAAATTTAGTCAAGATTTCTTAGACTGA 2820
2821 AAGAACCTTAAACAAAAAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAAT 2880
2821 AAGAACCTTAAACAAAAAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAAT 2880
2881 TTAATTTAGGCTTAATACATTTTCCCTATTTTCCATTTTCAATAAATGCTCTTAATACA 2940
2881 TTAATTTAGGCTTAATACATTTTCCCTATTTTCCATTTTCAATAAATGCTCTTAATACA 2940
2941 AAAAA 2945
2941 AAAAA 2945

[illegible]

polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukemia or lymphoma), inflammatory disease, necrosis, atherosclerosis, infertility, premature aging, psoriasis, inflammation, inflammatory disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence encodes a PRO polypeptide

SQ Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;

Query Match 100.0%; Score 2945; DB 7; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCGCCCGTCGCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60
DB 1 CGCTCGCCCGTCGCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60

QY 61 GGGTCAGCCCAACCGCGGGGACTATGGTGAATTCGCCGGCTCAGCACTACTGCCCT 120
DB 61 GGGTCAGCCCAACCGCGGGGACTATGGTGAATTCGCCGGCTCAGCACTACTGCCCT 120

QY 121 GATCGCGTCTTGTGGTCCCTCGGATCACCAATAGCATCGACTTCGGGGAGCAGGC 180
DB 121 GATCGCGTCTTGTGGTCCCTCGGATCACCAATAGCATCGACTTCGGGGAGCAGGC 180

QY 181 CTTGAACCGGGCATTTGCTGTCTCAAGGAGGATGCACTCGAGTCTGGCGACTACGG 240
DB 181 CTTGAACCGGGCATTTGCTGTCTCAAGGAGGATGCACTCGAGTCTGGCGACTACGG 240

QY 241 GCTGGCGTACTCCCTCATGAGTCTTCCAGGGTCCCATGAGTCACTCAAAATGTGGG 300
DB 241 GCTGGCGTACTCCCTCATGAGTCTTCCAGGGTCCCATGAGTCACTCAAAATGTGGG 300

QY 301 CTTGTGTGTTGTGAACAGCAAGAGAGACAGGACCAAGCCGCTCTGTGTATGGTGGC 360
DB 301 CTTGTGTGTTGTGAACAGCAAGAGAGACAGGACCAAGCCGCTCTGTGTATGGTGGC 360

QY 361 AGGGGCATCGTCCGCTTTTACACACTGATAGTATAGTATAGTATAGTATACAT 420
DB 361 AGGGGCATCGTCCGCTTTTACACACTGATAGTATAGTATAGTATAGTATACAT 420

QY 421 TATCAATAAATGCAACATGTGACGAGTCTGGGGAGCAAGACGAGAGGGCCCTTCT 480
DB 421 TATCAATAAATGCAACATGTGACGAGTCTGGGGAGCAAGACGAGAGGGCCCTTCT 480

QY 481 GTACCTCGCGCCCTTCTTTTATGACGCAATGGCATGGACCCCATGCTGGCATTTCTT 540
DB 481 GTACCTCGCGCCCTTCTTTTATGACGCAATGGCATGGACCCCATGCTGGCATTTCTT 540

QY 541 ABAACACAATACAGTTTCTGTTGGATGTGCTCAATCTCAGATGTATAGCTCAGGT 600
DB 541 ABAACACAATACAGTTTCTGTTGGATGTGCTCAATCTCAGATGTATAGCTCAGGT 600

QY 601 TGTGTTGTAGCCATTTGCTTCAAGTCACTGGAAATGCCGGAGCCCTGCTCATGCC 660
DB 601 TGTGTTGTAGCCATTTGCTTCAAGTCACTGGAAATGCCGGAGCCCTGCTCATGCC 660

QY 661 GATCCTCTCTGTATAGTGGGCACTTGTGGCTGCACACCCCTGTCTGGGCTACTA 720
DB 661 GATCCTCTCTGTATAGTGGGCACTTGTGGCTGCACACCCCTGTCTGGGCTACTA 720

QY 721 CAAGAACATTACGACATCATCCCTGACAGAGTGGCCCGAGCTGGGGGAGATCAAC 780
DB 721 CAAGAACATTACGACATCATCCCTGACAGAGTGGCCCGAGCTGGGGGAGATCAAC 780

QY 781 AATAAGAAAGATGCTGAGCTTCTGTGGCTTGGCTCTAATTCGGCCACACAGAGAT 840
DB 781 AATAAGAAAGATGCTGAGCTTCTGTGGCTTGGCTCTAATTCGGCCACACAGAGAT 840

QY 841 CAGTCGGCTATGTCAACCTCTTTTCCGGGACCTTGGTGGCAGTTCTGCGCCAC 900
DB 841 CAGTCGGCTATGTCAACCTCTTTTCCGGGACCTTGGTGGCAGTTCTGCGCCAC 900

QY 901 AGAGGAGTGGGATTTTACAGCCACATACCTGTGGGTCACTGCGCATAGCGTGT 960
DB 901 AGAGGAGTGGGATTTTACAGCCACATACCTGTGGGTCACTGCGCATAGCGTGT 960

QY 961 GAGGAAATCCGTCGTGTATCTCTGCTTTCAGCAAGATTAACCCAGCAACAACTGT 1020
DB 961 GAGGAAATCCGTCGTGTGTATCTCTGCTTTCAGCAAGATTAACCCAGCAACAACTGT 1020

QY 1021 GAGCAGAGCAACACAGTCAAGCCAGCCACATCAAGAAAGTTCACTTCTGTGCAATGGC 1080
DB 1021 GAGCAGAGCAACACAGTCAAGCCAGCCACATCAAGAAAGTTCACTTCTGTGCAATGGC 1080

QY 1081 TCTGTCACTCAGCTCTGTGTTTGTGATCTTTGGACACCAACGTTCTGAGAAATCTT 1140
DB 1081 TCTGTCACTCAGCTCTGTGTTTGTGATCTTTGGACACCAACGTTCTGAGAAATCTT 1140

QY 1141 GATAGACATCATCGAGTGGACTTTGCTTTTGCAAGAACTCTGTGTTTCTTTCGGAT 1200
DB 1141 GATAGACATCATCGAGTGGACTTTGCTTTTGCAAGAACTCTGTGTTTCTTTCGGAT 1200

QY 1201 CTTCTCTTCTTCCAGTTCAGTCAAGTGGGGGCACTCTACCGGTGGCTGATGAC 1260
DB 1201 CTTCTCTTCTTCCAGTTCAGTCAAGTGGGGGCACTCTACCGGTGGCTGATGAC 1260

QY 1261 ACTGAAGAAACCTTCTGCTTCTGCTCCCGAGCTCTGTGCTGCGATCATCTCTCATCGC 1320
DB 1261 ACTGAAGAAACCTTCTGCTTCTGCTCCCGAGCTCTGTGCTGCGATCATCTCTCATCGC 1320

QY 1321 CAGCTCTGCTGCTTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 CAGCTCTGCTGCTTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

QY 1381 CTTGCGGGCTTGTGGGAGAAATCCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 CTTGCGGGCTTGTGGGAGAAATCCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440

QY 1441 GAAGCAGAAAAAGATGGAGAAATGATCGGCCACGAGGGGGAAGACTCTGCCATGAC 1500
DB 1441 GAAGCAGAAAAAGATGGAGAAATGATCGGCCACGAGGGGGAAGACTCTGCCATGAC 1500

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DB 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGAGATGAATA 1560

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QY 1621 CTTCTCTCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680
DB 1621 CTTCTCTCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680

QY 1681 GGCCTTGATTTAAAGGTTTCTGTGCTCAATTTCTAGCATATGCGGTATGCTCACACTGACG 1740
DB 1681 GGCCTTGATTTAAAGGTTTCTGTGCTCAATTTCTAGCATATGCGGTATGCTCACACTGACG 1740

QY 1741 GGGGACCTAGTGAATGGTCTTTTCTGTTGTTTATGTTAAACAAACAAACAACTGACTT 1800
DB 1741 GGGGACCTAGTGAATGGTCTTTTCTGTTGTTTATGTTAAACAAACAAACAACTGACTT 1800

QY 1801 CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGGTGAGCTTGTGCTGCT 1860
DB 1801 CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGGTGAGCTTGTGCTGCT 1860

1861 TCCTCCCTGGCAAAATCTCTCTTGGAAACCAAGAGACTGAGCTGTGCCATCGCGCTCG 1920
Db
1861 TCCTCCCTGGCAAAATCTCTCTTGGAAACCAAGAGACTGAGCTGTGCCATCGCGCTCG 1920
Qy
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Db
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Qy
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Db
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Db
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Qy
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Db
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Db
2161 GACCTGTGACACAGCAGCTGACAGATGGAGAGTCTCCGTTAGAAAGTTTGGTTG 2220
Qy
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Db
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Db
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Qy
2881 TTAATTTAGGCTATAATACATTTCTTATTTTCCGATTTTCAATAAAATGCTCTTAATACA 2940
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Qy
2941 AAAAA 2945

Db 2941 AAAAA 2945
RESULT 9
ADA24545
ID ADA24545 standard; cDNA; 2945 BP.
XX
AC ADA24545;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO274 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;
chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder.
XX
OS Homo sapiens.
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978564.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
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PR 10-MAR-1998; 98US-0077450P.
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PR 26-MAR-1998; 98US-0079566P.
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PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
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PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087106P.
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PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	30-JUL-1998;	98US-0094651P.
PR	11-SEP-1998;	98US-0100038P.
PR	07-OCT-1998;	98WO-US021141.
PR	20-NOV-1998;	98US-0109304P.
PR	20-NOV-1998;	98WO-US024855.
PR	22-DEC-1998;	98US-0113296P.
PR	23-DEC-1998;	98US-01132621P.
PR	05-JAN-1999;	99WO-US000106.
PR	08-MAR-1999;	99WO-US0005028.
PR	10-MAR-1999;	99WO-US0005190.
PR	12-MAR-1999;	99US-0123957P.
PR	29-MAR-1999;	99US-0126773P.
PR	21-APR-1999;	99US-0130322P.
PR	26-APR-1999;	99US-0131022P.
PR	28-APR-1999;	99US-0131445P.
PR	14-MAY-1999;	99US-0134287P.
PR	14-MAY-1999;	99WO-US010733.
PR	02-JUN-1999;	99WO-US012252.
PR	16-JUN-1999;	99US-0139557P.
PR	23-JUN-1999;	99US-0141037P.
PR	07-JUL-1999;	99US-0142680P.
PR	26-JUL-1999;	99US-0145698P.
PR	28-JUL-1999;	99US-0146222P.
PR	29-OCT-1999;	99US-0162506P.
XX	(GETH) GENENTECH INC.	
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrera N, Filvaroff E, Pong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kljavin IJ, Luo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Stewart TA, Tumas D, Williams PM, Wood WI;	
XX	WPI; 2003-521814/49.	
XX	P-PSDB; ADA24546.	
XX	New isolated PRO polypeptides for example extracellular, secreted and membrane bound proteins, useful for modulating the biological activities of cells and for treating, for example diabetes, cancer, rheumatoid arthritis, and hearing loss.	
XX	Claim 2; Fig 3; 461pp; English.	
XX	The invention describes an isolated secreted and transmembrane (PRO) polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993 polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is useful for linking a bioactive molecule to a cell expressing a PRO337 polypeptide, and PRO337 is useful for linking a bioactive molecule to a cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739	
QY	Query Match 100.0%; Score 2945; DB 8; Length 2945;	
Db	Best Local Similarity 100.0%; Pred. No. 0;	
QY	Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 CGCTGCCCGTGCCTCCCTCCCTCCCGCAGAGTCCTCCGGGAGAGATGTGTG 60	
Db	1 CGCTGCCCGTGCCTCCCTCCCTCCCGCAGAGTCCTCCGGGAGAGATGTGTG 60	
QY	61 GGCTCACCCACGGCGGGACTATGTGAATTCCGGGGCTCACGCACTACTGGCCCT 120	
Db	61 GGCTCACCCACGGCGGGACTATGTGAATTCCGGGGCTCACGCACTACTGGCCCT 120	

QY 121 GATCCGGTCTTGGTGGCCCTGGGATCACCACATAGCCATCGACTTCGGGAGCAGGC 180
Db 121 GATCCGGTCTTGGTGGCCCTGGGATCACCACATAGCCATCGACTTCGGGAGCAGGC 180
QY 181 CTTGAACCGGGGATTCCTGCTGCTCAAGAGGATGAGTCGAGATGCTGGCAGCTACGG 240
Db 181 CTTGAACCGGGGATTCCTGCTGCTCAAGAGGATGAGTCGAGATGCTGGCAGCTACGG 240
QY 241 GCTGGCGTACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTGAATCAAAAATGTGG 300
Db 241 GCTGGCGTACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTGAATCAAAAATGTGG 300
QY 301 CTTGGTCTTTGTGAACAGAGAGAGACAGGACCAAGCCGTCTCTGTATGTGTGGTGGC 360
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QY 361 AGGGGCCATCGCTCCGCTTTTCACACACTGATAGCTTATAGTGAATTAGATACTACAT 420
Db 361 AGGGGCCATCGCTCCGCTTTTCACACACTGATAGCTTATAGTGAATTAGATACTACAT 420
QY 421 TATCAATAAACTGCACCATGTGACGAGTCGGTGGGAGCAAGACGAGAAAGGCCCTTCCT 480
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Db 541 AAAACACAAATACAGTTCCTGGTGGGATGTGCCTCAATCTCAGATGCTAGTCAAGGT 600
QY 601 TGTCTTTGTAGCCATTTTGTCTCAGTCACCTGGAAATGGGGAGCCCTGCTCATCCC 660
Db 601 TGTCTTTGTAGCCATTTTGTCTCAGTCACCTGGAAATGGGGAGCCCTGCTCATCCC 660
QY 661 GATCCTCTCTTTGACATGGCGCACTTGTGGCTGCACCAACCTGTGCTGGGCTACTA 720
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Db 721 CAAGAACATTCAGACATCATCCTGTGACAGAAAGTGGCCCGGAGCTGGGGGAGATGCAAC 780
QY 781 AATAAGAAAGATGCTGAGCTTCTGTGGCTTTTGGCTCTAATCTTGCCCAACAGAGAAAT 840
Db 781 AATAAGAAAGATGCTGAGCTTCTGTGGCTTTTGGCTCTAATCTTGCCCAACAGAGAAAT 840
QY 841 CAGTCGGCTATTGTCAACCTTTTGTTCGGGACCTTGGTGGCAGTTCGAGCCAC 900
Db 841 CAGTCGGCTATTGTCAACCTTTTGTTCGGGACCTTGGTGGCAGTTCGAGCCAC 900
QY 901 AGAGCAGTGGGATTTTGACGCCACATACCTGTGGGTCAATGCCATACGGCTGGTT 960
Db 901 AGAGCAGTGGGATTTTGACGCCACATACCTGTGGGTCAATGCCATACGGCTGGTT 960
QY 961 GACGAAATCCGTGCTGTGTATCTCTGCTTTTCGACAAAGAAATAACCCAGCAACAACTGGT 1020
Db 961 GACGAAATCCGTGCTGTGTATCTCTGCTTTTCGACAAAGAAATAACCCAGCAACAACTGGT 1020
QY 1021 GAGCAGGACACAGTCAGGCGACCCATCAGAGAAATCACTTCGTCTCATGGC 1080
Db 1021 GAGCAGGACACACAGTCAGGCGACCCATCAGAGAAATCACTTCGTCTCATGGC 1080
QY 1081 TCTGTCACTCAGCTCTGTCTGTATGTTTGGACACCCACCTGTCTGAGAAAATCTT 1140
Db 1081 TCTGTCACTCAGCTCTGTCTGTATGTTTGGACACCCACCTGTCTGAGAAAATCTT 1140
QY 1141 GATGACATCATCGAGTGACCTTTGCTTTCAGAACTCTGTGTGTCTTTGGGAT 1200
Db 1141 GATGACATCATCGAGTGACCTTTGCTTTCAGAACTCTGTGTGTCTTTGGGAT 1200
QY 1201 CTTCTCTCTTCCAGTTCAGTCAAGTGGGGCGCATCTCACCGGCTGGCTGATGAC 1260

Db 1201 CTTCTCTCTTCCAGTTCAGTCAAGTGGGGCGCATCTCACCGGCTGGCTGATGAC 1260
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Db 1261 ACTGAGAAAACCTTCCTTCCCTGGCCAGCTCTGTGCTGGGATCATGCTCTCATCGC 1320
QY 1321 CAGCCTCGTGTCTTACCTTACCTGGGGTGCACGGTCCGACCCCTGGGCGTGGCTCCCT 1380
Db 1321 CAGCCTCGTGTCTTACCTTACCTGGGGTGCACGGTCCGACCCCTGGGCGTGGCTCCCT 1380
QY 1381 CTTGGCGGCTTTGTGGGAGATCCACCTGGTCCCATCGCTGGTGTATGCTATCCG 1440
Db 1381 CTTGGCGGCTTTGTGGGAGATCCACCTGGTCCCATCGCTGGTGTATGCTATCCG 1440
QY 1441 GAAAGCAGAAAAGAGATGGAATGAGTCGGCCACGGAGGGGAAAGACTTCGCATGAC 1500
Db 1441 GAAAGCAGAAAAGAGATGGAATGAGTCGGCCACGGAGGGGAAAGACTTCGCATGAC 1500
QY 1501 AGACATGCTCCGACAGAGGAGTGACAGATCGTGGAAATGAGAGGAGATGAATA 1560
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QY 1981 CAGGTTAAACCTCGGCTTCTTTGATTTCTCCAGTCAATGGCCCTGACAAAGAGATG 2040
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QY 2161 GACCTGTACACAGAGGCTGACAGATGGAAGATCTCCCGTAGAAGGTTTGGTTG 2220
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QY 2221 AAATGCCCGGGGACGAAACTGACATGTTTGAATGATAGCATTTTCACTGCGTCTTC 2280
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Db	2281	CTAGATCTGACAAAGCTGTCTAGTTCTCACCCCCCGGTGTATATACATGAGCTAACTTTT	2340	PR	17-OCT-1997;	97US-0062250P.
Qy	2341	TTAAATTTGTACAAAAGCGCATCTCCAGATTCACAGACCCCTGCCGATGACTTTTCTCTGAA	2400	PR	03-NOV-1997;	97US-0064249P.
Db	2341	TTAAATTTGTACAAAAGCGCATCTCCAGATTCAGAGCCCTGCCGATGACTTTTCTCTGAA	2400	PR	13-NOV-1997;	97US-0065311P.
Qy	2401	GGCTTGCTTTTCCCTCGCTTCTCTGAGGTCGATTCAGAGCGAGTGCACATGAGAGATCC	2460	PR	21-NOV-1997;	97US-0066364P.
Db	2401	GGCTTGCTTTTCCCTCGCTTCTCTGAGGTCGATTCAGAGCGAGTGCACATGAGAGATCC	2460	PR	10-MAR-1998;	98US-0077450P.
Qy	2461	TAACTTTGCTTTTAACTTTTACAGTGAACCTGAAGCTTAAAGTCTCATCCAGATCTCAA	2520	PR	11-MAR-1998;	98US-0077632P.
Db	2461	TAACTTTGCTTTTAACTTTTACAGTGAACCTGAAGCTTAAAGTCTCATCCAGATCTCAA	2520	PR	11-MAR-1998;	98US-0077641P.
Qy	2521	TGCCAGGTTGCTGAGGTAATCTTTGAAGTAGATATATACCTGGTTCGCTATCCCTTA	2580	PR	12-MAR-1998;	98US-0077791P.
Db	2521	TGCCAGGTTGCTGAGGTAATCTTTGAAGTAGATATATACCTGGTTCGCTATCCCTTA	2580	PR	13-MAR-1998;	98US-0078004P.
Qy	2581	GTCTAATCTCGCGTACAGGTAATTTGAGATGTACTACGGTACTTCCCTCCACACCAT	2640	PR	20-MAR-1998;	98US-0078886P.
Db	2581	GTCTAATCTCGCGTACAGGTAATTTGAGATGTACTACGGTACTTCCCTCCACACCAT	2640	PR	20-MAR-1998;	98US-0078910P.
Qy	2641	ACGATAAAGCAAGACATTTTATAACGATACACAGATCACTATGTGTCTCTCCCTGAAATA	2700	PR	20-MAR-1998;	98US-0078938P.
Db	2641	ACGATAAAGCAAGACATTTTATAACGATACACAGATCACTATGTGTCTCTCCCTGAAATA	2700	PR	20-MAR-1998;	98US-0078938P.
Qy	2701	ACGATTCGAAATCGATCGAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTT	2760	PR	20-MAR-1998;	98US-0078939P.
Db	2701	ACGATTCGAAATCGATCGAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTT	2760	PR	25-MAR-1998;	98US-0079294P.
Qy	2761	CCTTTAAAAAATTTATACACCGGTTCTAATAATTTAGTACAGATTTCTAGACTGA	2820	PR	26-MAR-1998;	98US-0079566P.
Db	2761	CCTTTAAAAAATTTATACACCGGTTCTAATAATTTAGTACAGATTTCTAGACTGA	2820	PR	27-MAR-1998;	98US-0079663P.
Qy	2821	AAGAACCTTAAACAAAAAATTTTAAAGATATATAATATGCTGTATATGTATAT	2880	PR	27-MAR-1998;	98US-0079689P.
Db	2821	AAGAACCTTAAACAAAAAATTTTAAAGATATATAATATGCTGTATATGTATAT	2880	PR	27-MAR-1998;	98US-0079728P.
Qy	2881	TTATTTTAGGCTATATATATATTTTCCGATTTTCAATAAATGCTCTTAATACA	2940	PR	30-MAR-1998;	98US-0079920P.
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Qy	2941	AAAAA 2945		PR	31-MAR-1998;	98US-0080105P.
Db	2941	AAAAA 2945		PR	31-MAR-1998;	98US-0080107P.

RESULT 10
ACD29609
ID ACD29609 standard; cDNA; 2945 BP.
AC ACD29609;
XX ACD29609;
XX ACD29609;
DT 08-SEP-2003 (first entry)
DE Novel human secreted and transmembrane protein PRO274 cDNA.
XX Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
XX peripheral neuropathy; diabetic peripheral neuropathy;
KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW Refsum's disease; Abetalipoproteinemia; Tangier disease;
KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW Dejerine-Sottas syndrome; chromosome mapping; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003050240-A1.
XX
XX 13-MAR-2003.
XX
XX 16-OCT-2001; 2001US-00978403.
XX

PR	17-OCT-1997;	97US-0062250P.
PR	03-NOV-1997;	97US-0064249P.
PR	13-NOV-1997;	97US-0065311P.
PR	21-NOV-1997;	97US-0066364P.
PR	10-MAR-1998;	98US-0077450P.
PR	11-MAR-1998;	98US-0077632P.
PR	11-MAR-1998;	98US-0077641P.
PR	12-MAR-1998;	98US-0077791P.
PR	13-MAR-1998;	98US-0078004P.
PR	20-MAR-1998;	98US-0078886P.
PR	20-MAR-1998;	98US-0078910P.
PR	20-MAR-1998;	98US-0078938P.
PR	20-MAR-1998;	98US-0078939P.
PR	25-MAR-1998;	98US-0079294P.
PR	26-MAR-1998;	98US-0079566P.
PR	27-MAR-1998;	98US-0079663P.
PR	27-MAR-1998;	98US-0079689P.
PR	27-MAR-1998;	98US-0079728P.
PR	30-MAR-1998;	98US-0079920P.
PR	31-MAR-1998;	98US-0080105P.
PR	31-MAR-1998;	98US-0080107P.
PR	31-MAR-1998;	98US-0080165P.
PR	31-MAR-1998;	98US-0080194P.
PR	01-APR-1998;	98US-0080327P.
PR	01-APR-1998;	98US-0080328P.
PR	01-APR-1998;	98US-0080333P.
PR	08-APR-1998;	98US-0080334P.
PR	08-APR-1998;	98US-0081049P.
PR	08-APR-1998;	98US-0081070P.
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PR	08-APR-1998;	98US-0081195P.
PR	09-APR-1998;	98US-0081203P.
PR	09-APR-1998;	98US-0081229P.
PR	15-APR-1998;	98US-0081817P.
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PR	15-APR-1998;	98US-0081838P.
PR	15-APR-1998;	98US-0081952P.
PR	15-APR-1998;	98US-0081955P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082700P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082797P.
PR	22-APR-1998;	98US-0082804P.
PR	23-APR-1998;	98US-0082796P.
PR	27-APR-1998;	98US-0083366P.
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PR	29-APR-1998;	98US-0083582P.
PR	30-APR-1998;	98US-0083599P.
PR	05-MAY-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
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PR	07-MAY-1998;	98US-0084598P.
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PR	07-MAY-1998;	98US-0084637P.
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PR	07-MAY-1998;	98US-0084840P.
PR	13-MAY-1998;	98US-0084843P.
PR	13-MAY-1998;	98US-0085323P.
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Db 541 AAAACACAAATACAGTTCTCGTGGGATGTCCTCAATCTCAGATGTCATAGTCAAGT 600
Qy 601 TCTTTTGTAGCCATTTTGTTCACAGTCACTGGAATGCCGGAGCCCTGCTCATCCC 660
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Db |||||
QY 2941 AAAAA 2945
Db |||||
RESULT 11
ID ADA12206
AC ADA12206
XX AC ADA12206;
DT 06-NOV-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane polypeptide PRO274.
XX ss; gene; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human.
XX OS Homo sapiens.
XX PN US200305216-A1.
XX PD 20-MAR-2003.
XX PF 17-OCT-2001; 2001US-00378824.
XX PR 21-MAY-1996; 96US-0018049P.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-007450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079234P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
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PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
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PR 01-APR-1998; 98US-0080334P.
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PR 15-APR-1998; 98US-0081817P.
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XX (GETH) GENENTECH INC.
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KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
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KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease; Gene; ss.

XX Homo sapiens.

XX US2003049633-A1.

XX 13-MAR-2003.

XX 16-OCT-2001; 2001US-00978595.

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XX 03-NOV-1997; 97US-0064249P.

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KW	KW	Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;		
KW	KW	chromosome mapping; gene mapping; genetic disorder; septic shock;		
KW	KW	antibacterial; immunosuppressive; neuroprotective; gene; ss.		
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XX	PN	US2003045462-A1.		
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XX
AC ADB76228;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polynucleotide sequence #2.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
cell death; neuropathy; neuropathy related disease;
Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
chromosome mapping; gene mapping; genetic disorder; septic shock;
antibacterial; immunosuppressive; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003083248-A1.
XX
PD 01-MAY-2003.
XX
PF 16-OCT-2001; 2001US-00978757.
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AC ADC43654;
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DT 18-DEC-2003 (first entry)
DE Human cDNA encoding secreted/transmembrane protein, PRO274.
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW cytosolic; ophthalmological; antiarthritic; osteopathic; antirheumatic;
KW vulnary; auditory; tumor growth; retinal disorder;
KW sports-related joint problem; articular cartilage defects;
KW osteoarthritis; rheumatoid arthritis; wound healing; hearing loss.
XX
XX Homo sapiens.
XX
XX US2003054986-A1.
XX
PD 20-MAR-2003.
XX
XX 16-OCT-2001; 2001US-00981915.
XX
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Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A.

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JOURNAL Patent: WO 0153486-A 15 26-JUL-2001;
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Prediction of the coding sequences of unidentified human genes.
XVII. The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro
DNA Res. 7 (4), 273-281 (2000)
JOURNAL MEDLINE
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AUTHORS 2 (bases 1 to 328)
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Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdna@kazusa.or.jp,
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ORIGIN

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 AUTHORS Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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 Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
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 Carrinci, P., Prance, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:15778895.
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 Email: cgapsb-x@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadan@systemsbio.org
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AR243806
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DEFINITION Sequence 44 from patent US 6476195.
ACCESSION AR243806
VERSION AR243806.1 GI:27291299
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2572)
AUTHORS Komatsoulis, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A.,
Shi, Y., LaFleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P.,
Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and
Mucenski, M.
TITLE Secreted protein HNF6P20
JOURNAL Patent: US 6476195-A 44 05-NOV-2002;
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Query Match 79.2%; Score 2332.2; DB 6; Length 2572;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2345; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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FR	30-JUL-1998 US	60/09457,05-AUG-1998 US	60/095486 PR
OR	06-AUG-1998 US	60/095455,06-AUG-1998 US	60/095454 FR
PI	12-AUG-1998 US	60/096319	
PI	GEORGE A KOMATSOULIS,CRAIG A ROSEN,STEVEN M RUBEN,ROXANNE DUAN,		
PI	PAUL A MOORE,YANGGU SHI,DAVID LAFLEUR,YING PEI WEI,JIAN NI,P I KIMBERLY A FLORENCE,PAUL E YOUNG,LAURIE A BREWER,DANIEL R PI SOPPET,		
PI	GREGORY A ENDRESS,REINHARD EBNER,HENRIK S OLSEN,MICHAEL PI MUCENSKI		
PC	C12N15/09,A61K31/713,A61K38/00,A61K48/00,C07K14/47,C07K16/18, PC C12N1/15,		
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Query Match	79.2%; Score 2332.2; DB 6; Length 2572;		
Best Local Similarity	99.8%; Fred. No. 0;		
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RESULT 7
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LOCUS Homo sapiens cDNA FLJ27166 fis, clone SYN01530, highly similar to
DEFINITION Homo sapiens progressive ankylosis-like protein (ANK) mRNA.
ACCESSION AK130676
VERSION AK130676.1 GI:34527530
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Kanehori, K., Iehibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S.,
Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,
Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
Sugano, S.

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
NEDO human cDNA sequencing project	Unpublished	2 (bases 1 to 2152)	Sugano, S. and Suzuki, Y.		
Direct Submission					
Submitted (31-JUL-2003)	Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan				
(E-mail: fldcna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)					
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.					
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RESULT 8

BC009835

LOCUS

DEFINITION Homo sapiens ankylosis, progressive homolog (mouse), mRNA (CDNA clone MGC:15102 IMAGE:3927236), complete cds.

ACCESSION BC009835

VERSION BC009835.2 GI:33988513

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1892)

1 (bases 1 to 1892)

1 Krausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.D., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wexley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shavchenko, Y., Bouford, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, J., Smal, U., Schnerker, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

23388257

12477932

2 (bases 1 to 1892)

Strausberg, R.

Direct Submission

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 1892)

Strausberg, R.

Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Aug 20, 2003 this sequence version replaced gi:14602634.

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/brp

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadansystemsbio.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IMAGE Plate: 25 Row: b Column: 6

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536393.

FEATURES

Location/Qualifiers

1..1892

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/lab_host="DH10B-R_9"

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1..1892

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ORIGIN

Query Match 57.5%; Score 1692.4; DB 9; Length 1892;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCCGCCCGTCGCCCTCGCTCCCGCAGAGTCCCTCCCGCAGCAGATGTGTGTG 60

Db 175 CGTCCGCCCGTCGCCCTCGCTCCCGCAGAGTCCCTCCCGCAGCAGATGTGTG 234

Qy 61 GGGTCAGCCACCGGGGGAATATGTTGAATTCGGCGGCTCAGCAGTACTGCCCCCT 120

Db 235 GGGTCAGCCACCGGGGGAATATGTTGAATTCGGCGGCTCAGCAGTACTGCCCCCT 294

Qy 121 GATCCGGTTCCTGGTCCCTCCCGCATCACCAATAGCATTCGCGGAGCAGGC 180

Db 295 GATCCGGTTCCTGGTCCCTCCCGCATCACCAATAGCATTCGCGGAGCAGGC 354

Qy 181 CTTGAACCGGGGCAATTCGTGTCTCAAGGAGGATGCGTGCAGATGCTGCCAGCTACGG 240

Db 355 CTTGAACCGGGGCAATTCGTGTCTCAAGGAGGATGCGTGCAGATGCTGCCAGCTACGG 414

Qy 241 GCTGGGCTACTCCCTCATGAAGTCTTTCACGGGTCCTGAGTACTCAGAAATGTCGG 300

cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mcgenhri.nih.gov
Ahter.N., Ayele.K., Beckstrom-Sternberg.S.M., Benjamin.B.,
Blakesley.R.W., Bouffard.G.G., Breen.K., Brinkley.C., Brooks.S.,
Dierich.N.L., Granise.S., Guan.X., Gupta.J., Haghighi.P.,
Hansen.N., Ho.S.-L., Karlins.E., Kwong.P., Laric.P., Legaspi.R.,
Maduro.Q.L., Masello.C., Maskeri.B., Mastrian.S.D., McCloskey.J.C.,
McDowell.J., Pearson.R., Stantripop.S., Thomas.P.J., Touchman.J.W.,
Tsurgoeon.C., Vogt.J.L., Walker.M.A., Wetherby.K.D., Wiggins.L.,
Young.A., Zhang.L.-H. and Green.E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 116 Row: g Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9994166.

FEATURES

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/note="Vector: PCMV-SPORT6"

gene

1. .3468
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/db_xref="MGI:88023"

CDS

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SLTLCFVFWPTNVEKILIDIGVDFAPAECLVPLRIFSPFPVPTVRAHLTGWM
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ORIGIN

Query Match	53.8%;	Score 1585.2;	DB 10;	Length 3468;
Best Local Similarity	77.7%;	Pred. No. 0;		
Matches 2295;	Conservative	0;	Mismatches 468;	Indels 189;
Gaps	24;			
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Db	165	CTCGCGCGCTCCGACAGTGCCTCGCGCGCAGATGATGTGGGGTCAGCCAC	224	
QY	73	GGCGGGACTATGGTGAATTCCTCGCGCTCAGCAGTCTCGCGCTCAGTCCGCTTCT	132	
Db	225	GGCGGGACTATGGTGAATTCCTCGCGCTCAGCAGTCTCGCGCTCAGTCCGCTTCT	284	
QY	133	GGTGGCCCTGGGATCACCACATAGCCATTCGAGTTCGGGGAGCAGCCCTTGAACCGGG	192	
Db	285	GGTGGCCCTGGGATCACCACATAGCCATTCGAGTTCGGGGAGCAGCCCTTGAACCGGG	344	
QY	193	CATTGTGTCTCAAGAGAGATCAGTCAGATGCTGGCCAGCTACGGCTGGCGTACTC	252	
Db	345	CATCGCTGAGTCAAGAGAGATCAGTCAGATGCTGGCCAGCTACGGCTGGCGTACTC	404	

[illegible]

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Db	2489	TTTCTCTAACTGCTCAATTT	CGTTTTCACAGTGGAGAAAGCTTTTAAAGTCGTAATCTAGCAT	2548
Qy	2516	TCTAATGCCAGGTTGCTG	TAGGCTAACTTTTGAAGTAGATATATTACCTGGTTCTGCTAT	2575
Db	2549	CCTAATGCCAGGTTCTG	TCGTAACTTCGTATGATGTGCCGCTATTT-----	2601
Qy	2576	CCATTAGTCATAA	CTCTCGGTACAGGTAAATGGAAATGTACTACGGTACTTCCCTCCCCAC	2635
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Qy	2811	CCTAGACTGAAGAACCTTAAACAAAAA-AAATATTTTAAAGATATAAATATATCTGTATA	2869	
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Qy	2870	TGTTATGTAATTTATTTTAGGCTATAATACATTTCCATTTTCGATTTTCAATATAAAATG	2929	
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Qy	2930	TCTCTAATACAA	2941	
Db	2939	TCTCTAATACAA	2950	
RESULT 10				
LOCUS	AX698612	1568 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO02072079.			
ACCESSION	AX698612			PAT 02-APR-2003
VERSION	AX698612.1	GI:29499421		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	Nuernberg, P.			
TITLE	Agent for promoting bone formation and for use in osteoporosis therapy			
JOURNAL	Patent: WO 02072079-A 1 19-SEP-2002;			
FEATURES	Uni Charite Medizinische Fakultae der Humboldt-Uni zu Berlin (DE)			
source	Location/Qualifiers			
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Best Local Similarity	99.4%	Pred. No. 0		
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Db	1504	AGGAGGTGACAGACATCGTGGGAAATGACAGAGAGAGAAATGAATAAGGCACGGGACGCCAT	1563
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Db	1564	GG 1565	
RESULT 11			
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 1552, Conservative			
Query			
Db			
QY			
Db			

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1444 TGGAGAATAGTTCGCCACCGAGGGGAGAGCTTGGCCATGACAGACATGCTCTCGACAG 1503
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RESULT 12

AF274753 1568 bp mRNA linear PRI 27-JUL-2000
LOCUS Homo sapiens progressive ankylosis-like protein (ANK) mRNA,
DEFINITION complete cds.

AF274753
AF274753.1 GI:9502216

ACCESSION
AF274753

VERSION
AF274753.1

KEYWORDS
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 1568)

AUTHORS
Ho, A.M. Johnson, M.D. and Kingsley, D.M.

TITLE
Role of the mouse ank gene in control of tissue calcification and arthritis

JOURNAL
Science 289 (5477), 265-270 (2000)

MEDLINE
20355194

PUBMED
10894769

REFERENCE
2 (bases 1 to 1568)

AUTHORS
Kingsley, D.M., Ho, A.M. and Johnson, M.D.

TITLE
Submitted (05-JUN-2000) Department of Developmental Biology and

JOURNAL
Howard Hughes Medical Institute, Stanford University, Beckman

Center B300, Stanford, CA 94304-5327, USA

Location/Qualifiers

1. 1568

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69. 1547

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gene

CDS

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ORIGIN		Query Match	Score	1546.6;	DB 9;	Length	1568;
		Best Local Similarity	99.4%;	Pred. No. 0;			
		Mismatches	Conservative	0;	Mismatches	10;	Indels
		0; Gaps					
QY	18	CTGCGCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTGGGTGACGCCACGGCGG	77				
DB	4	CTCAGCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTGGGTGACGCCACGGCGG	63				
QY	78	GGACTATGGTGAATTCCTCCGCGCTCAGCAGTACTGGCCCTGATCCGGTCTTCTGGTGC	137				
DB	64	GGACTATGGTGAATTCCTCCGCGCTCAGCAGTACTGGCCCTGATCCGGTCTTCTGGTGC	123				
QY	138	CCCTGGGCATCAACAATAGCATCGACTTGGGAGAGAGCCCTTGAACCGGGGCAATTG	197				
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QY	198	CTGCTGCAAGGAGATGAGTGTGAGATGTGCGCAGCTACGGGCTGGGCTACTCCCTCA	257				
DB	184	CTGCTGCAAGGAGATGAGTGTGAGATGTGCGCAGCTACGGGCTGGGCTACTCCCTCA	243				
QY	258	TGAAGTTCTTTCAGCGGTPCCCATGAGTGAATTTCAAAAATGTGGGCCCTGGTGTGAA	317				
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QY	438	ATGTGGACAGTCCGTGGGAGCAGACGAGAGAGGCTTCTGTACCTCGCGCCCTTTC	497				
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QY	618	TGCTTCAGTCACTGGAATGCCGGAGCCCTGCTCATCCCGATCTCTCCTTGTACA	677				
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QY	678	TGGGCGCATTTGTGGCTGACCAACCTGTGCTGGGCTACTACAGAAATTCACAGCA	737				
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QY	738	TCATCCCTGACAGAGTGGCGGCTGGGGGAGATGCAACATTAAGAAGATGCTGA	797				
DB	724	TCATCCCTGACAGAGTGGCGGCTGGGGGAGATGCAACATTAAGAAGATGCTGA	783				
QY	798	GCTTCTGGTGGCTTTGGCTCTAATTTCTGGCCACACAGAGAAATCAGTCGGCTATTGCA	857				
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QY	858	ACCTCTTTGTTCCGGGACCTTGTGCGAGTTCTGACGCCACAGAGCAGTCGGGATTT	917				
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DB	1144	TGGACTTTGCTTGGAGAACTCTGTGTGTGTCTTTTGGGATCTTCTCTCTTCTCCAG	1203
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DB	1204	TTCCAGTCACAGTGGGGCGCATCTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCG	1263
QY	1278	TCCTTGGCCCGAGCTCTGTGTGGGATCATGTCCTCATCGCAGGCTCTGTGTCTTAC	1337
DB	1264	TCCTTGGCCCGAGCTCTGTGTGGGATCATGTCCTCATCGCAGGCTCTGTGTCTTAC	1323
QY	1338	CCTACTGGGGGTGCAGCGTGGACCCCTGGCGTGGGCTCCCTCTGCGGGGCTTTGTGG	1397
DB	1324	CCTACTGGGGGTGCAGCGTGGACCCCTGGCGTGGGCTCCCTCTGCGGGGCTTTGTGG	1383
QY	1398	GAGAAATCCACCATGCTGCCATCGTGTCTATGTCTACCGGAAGCAGAAAAGAGA	1457
DB	1384	GAGAAATCCACCATGCTGCCATCGTGTCTATGTCTACCGGAAGCAGAAAAGAGA	1443
QY	1458	TGGAGAAATGAGTCGCCACGAGGGGGAGAGCTTCCATGACAGACATGCTCCGACAG	1517
DB	1444	TGGAGAAATGAGTCGCCACGAGGGGGAGAGCTTCCATGACAGACATGCTCCGACAG	1503
QY	1518	AGGAGGTGACAGACATCGTGGAAATGAGAGAGGAGAAATGAATAGGCAACGGACG	1577
DB	1504	AGGAGGTGACAGACATCGTGGAAATGAGAGAGGAGAAATGAATAGGCAACGGACG	1563
QY	1578	GG 1579	
DB	1564	GG 1565	

RESULT 13

BD187384	2737 bp	DNA	linear	PAT 17-JUL-2003
Method for testing anti-osteoporosis agent.				
BD187384				
BD187384.1	GI:32997123			
VERSION	JP 2003009871-A/1.			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 2737)			
AUTHORS	Furukawa, H., Matsui, H., Kawaida, R. and Otsuka, T.			
TITLE	Method for testing anti-osteoporosis agent			
JOURNAL	Patent: JP 2003009871-A 1 14-JAN-2003;			
COMMENT	Sankyo Company Limited			
	OS Mus musculus			
	FN JP 2003009871-A/1			
	PD 14-JAN-2003			
	PI 14-JUN-2001 JP 2001180142			
	PI hidehiko furukawa,hideki matsui,remi kawaida,toshiaki otsuka			
	CC	Key	Location/Qualifiers	
	FR	CDS	(7):..(1482).	
	FT	Location/Qualifiers		

FEATURES

[illegible]

Qy	2115	GGTGGCAGCTGACGCGGAGTCCCGTTTCACACTGAGAAAGGAGACCTGTGACCACA	2174
Db	1940	GGCCCCAGGCTGACGCCCAAGTCTCCCTGTTCCAGAGAGGGGTGTGGCCCTGTG	1999
Qy	2175	GCAGGCTGACAGATGGACGAATCTCCCGTAGAAAGTGTGGTTGAAATGCCCGGGG	2234
Db	2000	GGCCACAGTAGTGGGAATTAATCTCTCTGTAGAAA-----TTGGGTCTAG	2043
Qy	2235	CAGCAAACTACATGTTGATGATAGCATTTCACTCTGGTCTCTCTAGATCTAGCAA	2294
Db	2044	TCACCAACTGACTGTATCGTTCAGCATCCCATGTTTTCCTGGTTTCACTGAGTTGCCGA	2103
Qy	2295	GCTGTGAGTTCTCACCCCAACCGGTATATACATGAGTCAACTTTTAAATTTGTCACAA	2354
Db	2104	-----CCCCACAGTGATATACATGAGTCACTTTTCAGAGCTGTCCCGC	2148
Qy	2355	AAGGCAATCTCCAGATTCACAGACCTCCCGCATGACATTTTCTGAAAGGCTGTGTTTCC	2414
Db	2149	AAGTGCAGCTCCAGTGTGACACACCT--CGCATGAGTTTCCCTGAAGGCTGTGGTTA-C	2206
Qy	2415	TCGCTTTTCTGGAAGTCGATATAGCGAGTACATGAGCATCTTAACCTTTGCAAT---	2471
Db	2207	TCGCTTCCCTGAAGATGGCAGTACAGCGAG--AAGTGAAGCGTTCTTAAGTGCATTTTC	2264
Qy	2472	-----TTTGTGTTTTACAGTAACTGAACTGTAAGCTTTTAACTCTCATCCAGCATTTA	2519
Db	2265	TCTAACTGTCCATTTCTGTTTTCACAGTGAGCAAAAGCTTTTAAAGTCGTAATCTAGCATCTTA	2324
Qy	2520	ATGCCAGTGTCTGAGGTAACTTTTGAAGTAGATATATTAAGTGTCTGCTATCCCT	2579
Db	2325	ATGCCAGGCTTGTCTCGTAACTTCTGATGTAGATGTGCGGCC-----	2368
Qy	2580	AGTCATAACTCTGGGTACAGGTAAATTTGAGAAATGTACTACGGTACTTCCCTCCACACCA	2639
Db	2369	-----TATTTCTGCAGCAGCAGGTAAACCGAG--TGTAAGTGTACTCCCTC-----CCA	2415
Qy	2640	TACGATAAGCAGACATTTTAT--AAGCATACAGAGTCACTATGTGGTCTCCCTGAAA	2698
Db	2416	CACCATTAAGCAAGACATTTTATAAACAGTATCAAGTCACTATGTGATAC--CCCGAAA	2474
Qy	2699	TAAAGCTTGGAAATCCATGCAAGTGCAGTATATTTTCTAAGTTTGGAAAGCAGGTTTT	2758
Db	2475	TAATGCTTGGAAATCCACTTAGTGAGTATATTTTCTAAGTTTGGAAAGCGGTTTT	2534
Qy	2759	TTCCCTTT-AAAAAATATAGACAGGTTCACTAAAT---TGATTTAGTCAGAAATTCCTTA	2814
Db	2535	TTCCCTTTAAAAAATATAGACAGTTCACATAATTCCTGATTTAGTCAAAAGTAACTA	2594
Qy	2815	GACTGAAAGAACCTTAAACAAAA--AAATATTTTAAAGATATAAATATATGCTATATGTT	2873
Db	2595	GACTGAAAGAACCTTAAACAAAAAATAATTTTAAAGATATAAATATATGCTATATGTT	2654
Qy	2874	ATGTAATTTATTTAGGCTATAATACATTTCTTATTTTCGATTTTCAATAAAATGCTC	2933
Db	2655	ATGTAATTTATTTAGGCTATAATACATTTCTTATTTTCGATTTTCAATAAAATGCTC	2714
Qy	2934	TAATACAAAAA 2945	
Db	2715	TAATACAAAAA 2726	

RESULT 14
AX698613
LOCUS AX698613 1562 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 2 from Patent WO202072079.
ACCESSION AX698613
VERSION AX698613.1 GI:29499422
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS	Nuernberg, P.		
TITLE	Agent for promoting bone formation and for use in osteoporosis therapy		
JOURNAL	Patent: WO 02072079-A 2 19-SEP-2002;		
FEATURES	Uni Charite Medizinische Fakultaeet der Humboldt-Uni zu Berlin (DE)		
source	Location/Qualifiers 1. 1562 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
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Query Match	51.6%; Score 1519.8; DB 6; Length 1562;		
Best Local Similarity	98.8%; Pred. No. 0;		
Matches 1543; Conservative	0; Mismatches 13; Indels 6; Gaps 1;		
Qy	18	CTCGGCTCCCGCAGAGTCCCTCGGGCAGCAGATGTGTGGGTGACGCCACCGCGG	77
Db	4	CTCAGCTCCCGCAGAGTCCCTCGGGCAGCAGATGTGTGGGTGACGCCACCGCGG	63
Qy	78	GGACTATGTTGAAATTCCTCGGGCGCTCAGCACTACTTGGGCCCTGATCCGGTTC	137
Db	64	GGACTATGTTGAAATTCCTCGGGCGCTCAGCACTACTTGGGCCCTGATCCGGTTC	123
Qy	138	CCCTGGGCATCACCACATAGCCATTCGACTTCGGGGAGCAGGCTTTGAACCGGGGCA	197
Db	124	CCCTGGGCATCACCACATAGCCATTCGACTTCGGGGAGCAGGCTTTGAACCGGGGCA	183
Qy	198	CTGCTGTCAAGAGGATGCAAGTGTGCCAGCTAGCGGGCTGGCGTACTCCTCTCA	257
Db	184	CTGCTGTCAAGAGGATGCAAGTGTGCCAGCTAGCGGGCTGGCGTACTCCTCTCA	243
Qy	258	TGAAGTTCTTCACGGGTCCCATGATGATCTTCAAAAATGTGGGCTGTGTTGTGAACA	317
Db	244	TGAAGTTCTTCACGGGTCCCATGATGATCTTCAAAAATGTGGGCTGTGTTGTGAACA	303
Qy	318	GCAAGAGACAGACCAAGCCGCTCTGTGTATGTGTGTGGCAGGGGCGATCGCTGCCG	377
Db	304	GCAAGAGACAGACCAAGCCGCTCTGTGTATGTGTGTGGCAGGGGCGATCGCTGCCG	363
Qy	378	TCCTTTCACACACTGATAGCTATTAGTGATTTAGGATCTACATATCAATAAAGTCAAC	437
Db	364	TCCTTTCACACACTGATAGCTATTAGTGATTTAGGATCTACATATCAATAAAGTCAAC	423
Qy	438	ATGTGGACAGTTCGGTGGGGAGCAAGACGAGAGGGCTTCCTGTACTCTCGCGCGCTTTC	497
Db	424	ATGTGGACAGTTCGGTGGGGAGCAAGACGAGAGGGCTTCCTGTACTCTCGCGCGCTTTC	483
Qy	498	CTTTCATGGAGCAATGGCATGGACCCATGCTGGCATTTCTTTAAACACAAATACAGTT	557
Db	484	CTTTCATGGAGCAATGGCATGGACCCATGCTGGCATTTCTTTAAACACAAATACAGTT	543
Qy	558	TCCTGGTGGGATGTGCTCAATCTCAGATGTCAAGTCTCAGGTTGTTTTGTAGCCATTT	617
Db	544	TCCTGGTGGGATGTGCTCAATCTCAGATGTCAAGTCTCAGGTTGTTTTGTAGCCATTT	603
Qy	618	TGCTTTCACAGTCACTGGAATGCGGGAGCCCTGCTCATCCGATCTCTCTCTGTGTACA	677
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Qy	678	TGGGCGCATTTGTGCGCTGCAACACCTGTGCTGGGCTACTACAAGAAATTCACGACA	737
Db	664	TGGGCGCATTTGTGCGCTGCAACACCTGTGCTGGGCTACTACAAGAAATTCACGACA	723
Qy	738	TCATCCCTGACAGAAAGTGGCCGAGCTGGGGGAGATGCACAATAAGAAAGATGCTGA	797
Db	724	TCATCCCTGACAGAAAGTGGCCGAGCTGGGGGAGATGCACAATAAGAAAGATGCTGA	783
Qy	798	GCTTCTGTGTGGCTTTTGGCTCTAATTTCTGGCCACACAGAGAAATCAGTCGGCTATTGTCA	857
Db	784	GCTTCTGTGTGGCTTTTGGCTCTAATTTCTGGCCACACAGAGAAATCAGTCGGCTATTGTCA	843
Qy	858	ACCTCTTTGTTTCCCGGGACCTTGGTGGCAGTTTCTGACGCCACAGAGCGAGTGGGATTT	917

Nuernberg, P.
Agent for promoting bone formation and for use in osteoporosis therapy
Patent: WO 02072079-A 2 19-SEP-2002;
Uni Charite Medizinische Fakultetaet der Humboldt-Uni zu Berlin (DE)
Location/Qualifiers
1. 1562
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Db 844 ACCTCTTTGTTCCGGGACCTTGGTGGAGTCTTGACGCCACAGAACAGTGGGATTT 903
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QY 978 TGTATCTCTGCTTTTCACAAAGATAACCCAGCAACAACTGGTGTGACGACGAAACACAG 1037
Db 964 TGTATCTCTGCTTTTCACAAAGATAACCCAGCAACAACTGGTGTGACGACGAAACACAG 1023
QY 1038 TCACGGCAGCCACATCAAGAAATTCACCTTCGTCTGATGCTCTGTCTACCTACGCTCT 1097
Db 1024 TCACGGCAGCCACATCAAGAAATTCACCTTCGTCTGATGCTCTGTCTACCTACGCTCT 1083
QY 1098 GTTTCGTGATGTTTGGACACCAACGCTGTCTGAGAAATCTTGTATGACATCATCGAG 1157
Db 1084 GTTTCGTGATGTTTGGACACCAACGCTGTCTGAGAAATCTTGTATGACATCATCGAG 1143
QY 1158 TGGACTTTGCCCTTTCAGAACTCTGTGTGTTTCCTTTGGGATCTTCTCTTCCCGAG 1217
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QY 1218 TTCCAGTCACAGTGAGGGCGCATCTCACGGGTGGCTGATGACACTGAAGAAACCTTCG 1277
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QY 1278 TCTTTCGCCCGAGCTGTGTGCGGATCATGCTCTCATGCCAGCTCTGTGTCCTAC 1337
Db 1258 TCTTTCGCCCGAGCTGTGTGCGGATCATGCTCTCATGCCAGCTCTGTGTCCTAC 1317
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QY 1398 GAGAAATCCACCATGTTGCGCATCTGCTGCTGTATGTCTACCGGAAGCAGAAAAAGAGA 1457
Db 1378 GAGAAATCCACCATGTTGCGCATCTGCTGCTGTATGTCTACCGGAAGCAGAAAAAGAGA 1437
QY 1458 TGGAGATGATCGCCACGAGGAGGAGAGACTCTGCCATGACACATGCTCTCCGACAG 1517
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QY 1578 GG 1579
Db 1558 GG 1559

RESULT 15
AC016649
LOCUS
DEFINITION Homo sapiens chromosome 5 clone RPI-14312, WORKING DRAFT SEQUENCE,
11 unordered pieces.
ACCESSION AC016649
VERSION AC016649.4 GI:13699598
KEYWORDS HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 165671)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165671)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Apr 20, 2001 this sequence version replaced gi:7711590.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 193053
Center clone name: RPCI-1_14312

Summary Statistics
Consensus quality: 152857 bases at least Q40
Consensus quality: 156684 bases at least Q30
Consensus quality: 157624 bases at least Q20
Estimated insert size: 154000; pulse field gel estimation
Quality coverage: 5.96 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.57 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1134: contig of 1134 bp in length
* 1135 1234: gap of unknown length
* 1235 2945: contig of 1711 bp in length
* 2946 3045: gap of unknown length
* 3046 4302: contig of 1257 bp in length
* 4303 4402: gap of unknown length
* 4403 5439: contig of 1036 bp in length
* 5439 7157: gap of unknown length
* 7158 7257: contig of 1619 bp in length
* 7258 9959: gap of unknown length
* 9959 11943: contig of 1985 bp in length
* 11944 12043: gap of unknown length
* 12044 21909: contig of 9866 bp in length
* 21910 22009: gap of unknown length
* 22010 40513: contig of 18404 bp in length
* 40514 68716: gap of unknown length
* 68717 68816: gap of unknown length
* 68817 165671: contig of 96855 bp in length.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="RPI-14312"
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ORIGIN
Query Match 50.7%; Score 1493.2; DB 2; Length 165671;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1446 AGAAAAAGAGATGGAGATGAGTGGCCACGAGGGGAGACTCTGCCATGACAGACA 1505
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QY 1506 TGCCTCCGACAGAGAGGAGTGCACAGACATCTGTGGAATGAGAGAGGAGAAATAGGCA 1565
Db 129600 TGCCTCCGACAGAGAGGAGTGCACAGACATCTGTGGAATGAGAGAGGAGAAATAGGCA 129659
QY 1566 CGGACGCCATGGGCACTGACGGGACGGTCAAGTACAGACTTCGGCATCATCTCTT 1625
Db 129660 CGGACGCCATGGGCACTGACGGGACAGTCAAGTACAGACTTCGGCATCATCTCTT 129719

